

AMENDMENTS TO THE SPECIFICATION

Please amend the specification as described below.

Delete paragraphs 0058-0096.

Replace paragraph 0155 with the following paragraph.

The nucleotide sequences of each of a plurality of GAM oligonucleotides that are described by Fig. 1 and their respective genomic sources and genomic locations are set forth in Tables 1-3, hereby incorporated herein. Specifically, in Table 1, line 778 describes GAM RNA (miRNA) as set forth in SEQ ID NO: 348 is shown as predicted from human.

After paragraph 0155, add the following Table 1, paragraph, Table 2, paragraph, and Table 3.

Table 1

GAM SEQ-ID	GAM NAME	GAM RNA SEQUENCE	GAM ORGANISM	GAM POS
=====	=====	=====	=====	=====
348	GAM353678	CAGCAGCACACTGTGGTTGTA	Human	A

In Table 2, lines 42112-42207, describes GAM PRECURSOR RNA (hairpin) as set forth in SEQ ID NO: 4233864 and as it relates to Figures 1-8 .

Table 2

GAM NAME	GAM ORGA NISM	PRECUR SEQ-ID	PRECURSOR SEQUENCE	GAM DESCRIPTION
-----	-----	-----	-----	-----
GAM 353678	Human	4233 864	CCTGCTCCCG CCCCAGCAGC ACACTGTGGT TTGTACGGCA CTGTGGCCAC GTCCAAACCA CACTGTGGTG TTAGAGCGAG GGTGGGGGAGG	Fig. 1 further provides a conceptual description of another novel bioinformatically-detected human oligonucleotide of the present invention referred to here as the Genomic Address Messenger 353678 (GAM353678) oligonucleotide, which modulates expression of respective target genes whose function and utility are known in the art. GAM353678 is a novel bioinformatically detectable regulatory, non-

protein-coding, miRNA-like oligonucleotide. The method by which GAM353678 is detected is described with additional reference to Figs. 1-8. The GAM353678 precursor, herein designated GAM PRECURSOR, is encoded by the Human genome. GAM353678 target gene, herein designated GAM TARGET GENE, is a target gene encoded by the target organism as specified in Tables 6-7. The GAM353678 precursor, herein designated GAM PRECURSOR, encodes a GAM353678 precursor RNA, herein designated GAM PRECURSOR RNA. Similar to other miRNA oligonucleotides, the GAM353678 precursor RNA does not encode a protein. GAM353678 precursor RNA folds onto itself, forming GAM353678 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA, which has a two-dimensional "hairpin" structure. GAM PRECURSOR RNA folds onto itself, forming GAM FOLDED PRECURSOR RNA, which has a two-dimensional "hairpin structure". As is well-known in the art, this "hairpin structure" is typical of RNA encoded by known miRNA precursor oligonucleotides and is due to the full or partial complementarity of the nucleotide sequence of the first half of an miRNA precursor to the RNA that is encoded by a miRNA oligonucleotide to the nucleotide sequence of the second half thereof. A nucleotide sequence that is identical or highly similar to the nucleotide sequence of the GAM353678 precursor RNA is designated SEQ ID NO:4233864, and is provided hereinbelow with reference to the sequence listing section. The nucleotide sequence designated SEQ ID NO:4233864 is located from position 7121806 to position 7121896 relative to chromosome 17 on the "-" strand, and overlaps an intergenic region (UCSC.h16.refGene database). Furthermore, the nucleotide sequence designated SEQ ID NO:4233864 is positioned in a region that is conserved

between human, mouse and rat (UCSC.hg16.humorMm3Rn3). A schematic representation of a predicted secondary folding of GAM353678 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA is set forth in Table 4 incorporated herein. An enzyme complex designated DICER COMPLEX, an enzyme complex composed of Dicer RNaseIII together with other necessary proteins, cuts the GAM353678 folded precursor RNA yielding a single-stranded ~22 nt-long RNA segment designated GAM353678 RNA, herein designated GAM RNA. Table 5 provides a nucleotide sequence that is highly likely to be identical or extremely similar to the nucleotide sequence of GAM353678 RNA, hereby incorporated herein. GAM353678 target gene, herein designated GAM TARGET GENE, encodes a corresponding messenger RNA, designated GAM353678 target RNA, herein designated GAM TARGET RNA. As is typical of mRNA of a protein-coding gene, GAM353678 target RNA comprises three regions, as is typical of mRNA of a protein-coding gene: a 5' untranslated region, a protein-coding region and a 3' untranslated region, designated 5'UTR, PROTEIN-CODING and 3'UTR, respectively. GAM353678 RNA, herein designated GAM RNA, binds complementarily to one or more target binding sites located in the untranslated regions of GAM353678 target RNA. This complementary binding is due to the partial or full complementarity between the nucleotide sequence of GAM353678 RNA and the nucleotide sequence of each of the target binding sites. As an illustration, Fig. 1 shows three such target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III, respectively. It is appreciated that the number of target binding sites shown in Fig. 1 is only illustrative and that any suitable number of target binding sites may be present. It is further appreciated that although Fig.

1 shows target binding sites only in the 3'UTR region, these target binding sites may instead be located in the 5'UTR region or in both the 3'UTR and 5'UTR regions. The complementary binding of GAM353678 RNA, herein designated GAM RNA, to target binding sites on GAM353678 target RNA, herein designated GAM TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits the translation of GAM353678 target RNA into respective GAM353678 target protein, herein designated GAM TARGET PROTEIN, shown surrounded by a broken line. It is appreciated that the GAM353678 target gene, herein designated GAM TARGET GENE, in fact represents a plurality of GAM353678 target genes. The mRNA of each one of this plurality of GAM353678 target genes comprises one or more target binding sites, each having a nucleotide sequence which is at least partly complementary to GAM353678 RNA, herein designated GAM RNA, and which when bound by GAM353678 RNA causes inhibition of translation of the GAM353678 target mRNA into a corresponding GAM353678 target protein. The mechanism of the translational inhibition that is exerted by GAM353678 RNA, herein designated GAM RNA, on one or more GAM353678 target genes, herein collectively designated GAM TARGET GENE, may be similar or identical to the known mechanism of translational inhibition exerted by known miRNA oligonucleotides. The nucleotide sequence of GAM353678 precursor RNA, herein designated GAM PRECURSOR RNA, its respective genomic source and genomic location and a schematic representation of a predicted secondary folding of GAM353678 folded precursor RNA, herein designated GAM FOLDED PRECURSOR RNA are set forth in Tables 3-4, hereby incorporated herein. The nucleotide sequences of a "diced" GAM353678 RNA, herein

designated GAM RNA, from GAM353678 folded precursor RNA are set forth in Table 5, hereby incorporated herein. The nucleotide sequences of target binding sites, such as BINDING SITE I, BINDING SITE II and BINDING SITE III of Fig. 1, found on GAM353678 target RNA, herein designated GAM TARGET RNA, and a schematic representation of the complementarity of each of these target binding sites to GAM353678 RNA, herein designated GAM RNA, are set forth in Tables 6-7, hereby incorporated herein. It is appreciated that the specific functions and accordingly the utilities of GAM353678 RNA are correlated with and may be deduced from the identity of the GAM353678 target gene inhibited thereby, and whose functions are set forth in Table 8, hereby incorporated herein.

Table 3, lines 1279-1280, shows data relating to the source and location of the GAM oligonucleotide, specifically the GAM PRECRSOR (hairpin) and its position in the genomic sequence of human.

Table 3

GAM NAME	PRECUR SOR SEQ-ID	GAM ORGANISM	SOURCE	STR AND	SRC-START OFFSET	SRC-END OFFSET
-----	-----	-----	-----	---	-----	-----
GAM353678	4233864	Human	17	---	7121806	7121896

Replace paragraph 0156 with the following paragraph.

The nucleotide sequences of GAM PRECURSOR RNAs, and a schematic representation of a predicted secondary folding of GAM FOLDED PRECURSOR RNAs, of each of a plurality of GAM oligonucleotides described by Fig. 1 are set forth in Table 4, hereby incorporated herein. Table 4 lines 2384-2388, shows a schematic representation of the GAM folder precursor as set forth in SEQ ID NO:348, beginning at the 5' end (beginning of upper row) to the 3'

end (beginning of lower row), where the hairpin loop is positioned at the right part of the drawing.

After paragraph 0156, add the following Table 4.

Table 4

GAM NAME	PRE CUR SEQ -ID	GAM ORGA NISM	PRECURSOR SEQUENCE	GAM FOLDED PRECURSOR RNA									
-----	-----	-----	-----	-----									
GAM	423	Human	CCTGCTCCGCCCCASCAGC	G	C-----	G	C	T	--	AC			
353	386		ACACTGTGGTTTGTACGGCA	CCT	CTCCGGCC	AGCA	GACA	TGTGGTTTG	AC	GGC	T		
678	4		CTGTGGCCACGTCCAAACCA	GGA	GGGGTGGG	TTGT	GTGT	ACACCAAAC	TG	CCG	G		
			CACTGTGGTGTAGACGAG	-	AGCGAGA	G	C	C	CA	GT			
			GCTGGGGAGS										

Replace paragraph 0157 with the following paragraph.

The nucleotide sequences of “diced” GAM RNAs of each of a plurality of GAM oligonucleotides described by Fig. 1 are set forth in Table 5, hereby incorporated herein. Table 5, line 1276 shows the mature GAM RNA as set forth in SEQ ID NO: 348 as sliced by DICER from the GAM PRECURSOR sequence (hairpin) as set forth in SEQ ID NO: 4233864.

After paragraph 0157, add the following Table 5.

GAM NAME	GAM ORGANISM	GAM RNA SEQUENCE	PRECUR SEQ-ID	GAM POS
-----	-----	-----	-----	-----
GAM353678	Human	CAGCAGCACACTGTGGTTTGA	4233864	A

Replace paragraph 0158 with the following paragraph.

The nucleotide sequences of target binding sites, such as BINDING SITE I, BINDING SITE II and BINDING SITE III that are found on GAM TARGET RNAs of each of a plurality of GAM oligonucleotides that are described by Fig. 1, and a schematic representation of the complementarity of each of these Target binding sites to each of a plurality of GAM RNAs that are described by Fig. 1 are set forth in Tables 6-7, hereby incorporated herein. Table 6 shows data relating to the SEQ ID NO of the GAM target binding site sequence of the target gene name as bound by the GAM RNA as set forth in SEQ ID NO: 348. Table 6, lines 3688165, 767082, 762322 and 763042 related to target binding site SEQ ID NO: 1810388, 673420, 671402 respectively.

After paragraph 0158, add the following Table 6, paragraph, and Table 7.

Table 6

TARGET BINDING SITE SEQ-ID	TARGET ORGANISM	TARGET	TARGET BINDING SITE SEQUENCE
1810388	Human	MGAT5	CACCATGCTGCTG
673420	Human	SERPINH1	AAACTAGGTGCTGCAG
671402	Human	SERPINH1	ATACCATGATGCTG
671042	Human	SERPINH1	CTATAAACTAGGTGCTGCAG

Table 7, lines 312839-313773 shows data relating to target genes and binding site of GAM oligonucleotides.

Table 7

GAM NAME	GAM ORGA NISM	GAM RNA SEQUENCE	TARGET BS-SEQ	TARG ET	TARGET REF-ID	TARGET ORGANISM	UTR	BINDING SITE (UPPER:TARGET;LOWER:GAM)	DRAW	GAM POS
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	AAACCAAA CTTATGCA GCTG	nup C	NC_004431 f rom 27953 90 to 27966 31 (+)	Escher ichia coli CFT073	3 ---	A C TA A A A C C A A C G C C -	A	A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	AAACCAAA CTTATGCA GCTG	nup C	NC_004741 f rom 24940 19 to 24952 21 (+)	Shigella flexneri 2a str . 2457T	3 ---	A C TA A A A C C A A C G C C -	A	A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTA	AAACCCCTG CTGCG	rel A	NC_000962 f rom 29078 24 to 29101 96 (-)	Mycobacterium tuberculosis H37Rv	3 ---	C----- A A A C C T G T G C G T T T T G T G T C A C G C A	A	A

GAM35	Hum	CAGCAGCA	AAACCCCTG	rel	NC_002945	Mycobac	3	---	C-----	-	A
3678	an	CACTGTGG	CTGCG	A	rom 28752	teriu m			AAACC	TGCTGC	G
		TTTGTA			74 to 28776	bovis			TTTGG	ACGACG	C
					46 (-)	subs p			ATG	TGTCAC	A
						bovis					
						AF21					
						22/97					
GAM35	Hum	CAGCAGCA	AAACCCCTT	yab	NC_004431	Escheri	3	---	C TTC-	T	A
3678	an	CACTGTGG	TCTGTGTC	O	rom 614	chia			AAACC	T	TGCTGCT
		TTTGTA	TT		89 to 62148	coli			TTTGG	G	ACGACG
					(-)	CFT073			ATG	T	TCAC
GAM35	Hum	CAGCAGCA	AAACCGAT	amt	NC_004337	Shigell	3	---	AT CAG	G	A
3678	an	CACTGTGG	GCAGTGGC	B	rom 4080	a file			AAACCG	G	TGC GCTG
		TTTGTA	GCTG		59 to 40934	xneri			TTTGG	C	ACG CGAC
					5 (+)	2a str			ATG	GT AC-	A
						. 301					
GAM35	Hum	CAGCAGCA	AAACCGAT	amt	NC_004741	Shigell	3	---	AT CAG	G	A
3678	an	CACTGTGG	GCAGTGGC	B	rom 4078	a file			AAACCG	G	TGC GCTG
		TTTGTA	GCTG		60 to 40914	xneri			TTTGGT	C	ACG CGAC
					6 (+)	2a str			ATG	GT AC-	A
						. 2457T					
GAM35	Hum	CAGCAGCA	AAACCGAT	amt	NC_004431	Escheri	3	---	AT CCG	G	A
3678	an	CACTGTGG	GCCTGTGG	B	rom 5476	chia			AAACCG	G	TGC GCTG
		TTTGTA	GCTG		16 to 54890	coli			TTTGGT	C	ACG CGAC
					2 (+)	CFT073			ATG	GT AC-	A
GAM35	Hum	CAGCAGCA	AAACCGCC	dsd	NC_003197	Salmone	3	---	CCCCAG	-	A
3678	an	CACTGTGG	CCCAGTCT	A	rom 40044	lla t			AAACCGC	T	
		TTTGTA	GCTG		53 to 40057	yphimur			CTGCTG	TTTGGT	
					75 (+)	ium L			A	GACGAC	ATG
						T2			TCAC--	C	
GAM35	Hum	CAGCAGCA	AAACCGCC	gad	NC_002947	Pseudom	3	---	GCC -	C	A
3678	an	CACTGTGG	CTTGCCGC		rom 48716	onas			AAACCG	T	TGC GCTG
		TTTGTA	TG		25 to 48729	putida			TTTGGT	A	ACG CGAC
					29 (+)	KT244 0			ATG	GTC C	A
GAM35	Hum	CAGCAGCA	AAACGAAT	aro	NC_003116	Neisser	3	---	G ATGAAATCA	C	A
3678	an	CACTGTGG	TGAATCAT	A	rom 15575	ia me			AAAC	A	TCG
		TTTGTA	GCCGCTG		02 to 15588	ningiti			GCTG	TTTG	T
					03 (+)	dis 2				ACG CGAC	ATG
						2491			G	GTCAC----	A
GAM35	Hum	CAGCAGCA	AAACGACG	ruv	NC_003143	Yersini	3	---	G ---G	AAAC	A
3678	an	CACTGTGG	GGCTGCTG	B	rom 23364	a pes			ACG	GCTGCTG	TTTG
		TTTGTA			49 to 23374	tis			TGT	CGACGAC	ATG
					53 (+)				CACA		
GAM35	Hum	CAGCAGCA	AAACGACG	ruv	NC_004088	Yersini	3	---	G ---G	AAAC	A
3678	an	CACTGTGG	GGCTGCTG	B	rom 24820	a pes			ACG	GCTGCTG	TTTG
		TTTGTA			31 to 24830	tis KIM			TGT	CGACGAC	ATG
					35 (-)				CACA		
GAM35	Hum	CAGCAGCA	AAACGATA	ycl	NC_004431	Escheri	3	---	G ---C	-	A
3678	an	CACTGTGG	TCTGTGCTG	E	rom 15586	chia			AAAC	ATA	T
		TTTGTA			41 to 15591	coli			TTTG	TGT	A
					47 (-)	CFT073			ATG	G	CAC C
GAM35	Hum	CAGCAGCA	AAACGCAI	van	NC_002516	Pseudom	3	---	G	T CA	-
3678	an	CACTGTGG	GTTCATGC	B	rom 55041	onas			AAAC	CATG	T
		TTTGTA	GCTG		20 to 55050	aerugin			GCTG	TTTG	TGT
					73 (+)	osa P			ACG	CGAC	ATG
						A01			C-	A	
GAM35	Hum	CAGCAGCA	AAACGCTC	fts	NC_000922	Chlamyd	3	---	GC	CCGTAATAC	A
3678	an	CACTGTGG	CGTATACT	Y	rom 11154	ophil a			A	AAAC	T

	TTTGTA	GCTGCTA	27 to 11162	pneumon		TGCTGCT	TTTG	
			99 (-)	iae	G	ACGACGA	ATG	
				CWL029		GT TCAC----	C	
GAM35	Hum	CAGCAGCA	NC_002491 f	Chlamy	3	GC CCGTATAC		A
3678	an	CACTGTGG	rom 11131	ophil a		A AAAC T		
		TTTGTA	27 to 11139	pneumon		TGCTGCT	TTTG	
			99 (-)	iae	G	ACGACGA	ATG	
				J138		GT TCAC----	C	
GAM35	Hum	CAGCAGCA	NC_004337 f	Shigell	3	ATCGACAGT		A
3678	an	CACTGTGG	rom 39477	a file		AAACTA		
		TTTGTA	08 to 39487	xneri		TGCTGC G		
			00 (+)	2a str		TTTGGT		
				. 301		ACGACG C	ATG	
						GTAC----	A	
GAM35	Hum	CAGCAGCA	NC_004741 f	Shigell	3	ATCGACAGT		A
3678	an	CACTGTGG	rom 38245	xneri		AAACTA		
		TTTGTA	94 to 38255	2a str		TGCTGC G		
			77 (-)	. 2457T		TTTGGT		
						ACGACG C	ATG	
						GTAC----	A	
GAM35	Hum	CAGCAGCA	SER		3	G ---		A
3678	an	CACTGTGG	PIN NM_001235	Human		AAACTA G	TGCTGC G	
		TTTGTA	H 1			TTTGGT T	ACGACG C	
						ATG	G CAC	A
GAM35	Hum	CAGCAGCA	NC_004337 f	Shigell	3	T G C GCAA		A
3678	an	CACTGTGG	rom 15575	a file		AAAC CA G TG		
		TTTGTA	27 to 15585	xneri		GCTGCTG	TTTG GT T	
			73 (-)	2a str	AC	CGACGAC	ATG	-
				. 301	G C	---A		
GAM35	Hum	CAGCAGCA	NC_003197 f	Salmone	3	G -----		T A
3678	an	CACTGTGG	rom 43877	lla t		AAA C	TGCTGCT	
		TTTGTA	27 to 43881	yphimur		TTT G	ACGACGA	
			82 (-)	ium L		ATG	G TGTCAC	C
				T2				
GAM35	Hum	CAGCAGCA	NC_003197 f	Salmone	3	GTGTACT T		A
3678	an	CACTGTGG	rom 25516	lla t		AAATCA	TG	
		TTTGTA	51 to 25525	yphimur		TGCTG	TTTGGT	
			62 (-)	ium L		AC ACAC	ATG	
				T2		GTAC----	G	
GAM35	Hum	CAGCAGCA	NC_004431 f	Escheri	3	- - - - -	AA C	A
3678	an	CACTGTGG	rom 44392	chia		AT	TGCTGCT	TT G
		TTTGTA	60 to 44402	coli		TG	ACGACGAC	ATG T G
			52 (+)	CFT073		TCAC		
GAM35	Hum	CAGCAGCA	NC_003197 f	Salmone	3	- - - - -		C A
3678	an	CACTGTGG	rom 43430	lla t		AA C	TGCTGCT	
		TTTGTA	80 to 43439	yphimur		TT G	ACGACGA	
			97 (+)	ium L		ATG	T TGTCAC	C
				T2				
GAM35	Hum	CAGCAGCA	NC_003198 f	Salmone	3	- - - - -		C A
3678	an	CACTGTGG	rom 36072	nterica		AA C	TGCTGCT	
		TTTGTA	04 to 36081	ente		TT G	ACGACGA	
			21 (-)	rica		ATG	T TGTCAC	C
				serovar				
				Typhi				
GAM35	Hum	CAGCAGCA	NC_004631 f	Salmone	3	- - - - -		C A
3678	an	CACTGTGG	rom 35928	nterica		AA C	TGCTGCT	
		TTTGTA	64 to 35937	ente		TT G	ACGACGA	
			81 (-)	rica		ATG	T TGTCAC	C
				serovar				

				Typhi			
				Ty2			
GAM35	Hum	CAGCAGCA	AAGCCGGT	aro	NC_003116 f	Neisser	3
3678	an	CACTGTGG	TGCGGTGC	A	rom 15575	ia me	AAGCCG
		TTTGTA	TGCTG		02 to 15588	ningiti	TGCTGTG
					03 (+)	dis 7	TTTGGT
						2491	ACGACGA ATG
							GTCAC--
				Salmone			
GAM35	Hum	CAGCAGCA	AATCCACT	glg	NC_003198 f	lla e	3
3678	an	CACTGTGG	CCGTGTG	P	rom 41445	nterica	--- T TCC T AA
		TTTGTA	CTG		68 to 41470	ente	CCAC GTG TGCTG TT
					15 (+)	rica	GGTG CAC ACGAC ATG T
						serovar	TCA G
				Typhi			
				Salmone			
GAM35	Hum	CAGCAGCA	AATCCACT	glg	NC_004631 f	lla e	3
3678	an	CACTGTGG	CCGTGTG	P	rom 41292	nterica	--- T TCC T AA
		TTTGTA	CTG		15 to 41316	ente	CCAC GTG TGCTG TT
					62 (+)	rica	GGTG CAC ACGAC ATG T
						serovar	TCA G
				Typhi			
				Ty2			
GAM35	Hum	CAGCAGCA	ACATGCTG	nup	NC_004431 f	Escheri	3
3678	an	CACTGTGG	CTT	C	rom 27953	chia	--- A C A TGCTGCT T
		TTTGTA			90 to 27966	coli	T G T ACGACGA
					31 (+)	CFT073	ATG TT G GTCAC C
				Shigell			
GAM35	Hum	CAGCAGCA	ACATGCTG	nup	NC_004741 f	a file	3
3678	an	CACTGTGG	CTT	C	rom 24940	xneri	--- A C A TGCTGCT T
		TTTGTA			19 to 24952	2a str	T G T ACGACGA
					21 (+)	. 2457T	ATG TT G GTCAC C
				Mycobac			
GAM35	Hum	CAGCAGCA	ACGATGGT	pho	NC_000962 f	teriu m	3
3678	an	CACTGTGG	GCTT	Y2	rom 9135	tubercu	--- -- G TAC
		TTTGTA			56 to 91419	los is	T T A C ATGGTG A
					7 (-)	H37Rv	TGCTGCT T G
							TGTCAC ACGACGA ATG TT
							G --- C
				Mycobac			
GAM35	Hum	CAGCAGCA	ACGATGGT	pho	NC_002945 f	teriu m	3
3678	an	CACTGTGG	GCTT	Y2	rom 9143	bovis	--- -- G TAC
		TTTGTA			88 to 91502	subs p	T T A C ATGGTG A
					9 (-)	bovis	TGCTGCT T G
						AF21	TGTCAC ACGACGA ATG TT
						22/97	G --- C
				Salmone			
GAM35	Hum	CAGCAGCA	ACTGCTGC	glg	NC_003198 f	lla e	3
3678	an	CACTGTGG	TC	P	rom 41445	nterica	--- -- ----- C
		TTTGTA			68 to 41470	ente	A C TGCTGCT A
					15 (+)	rica	T G ACGACGA
						serovar	ATG TT GTGTCAC C
				Typhi			
				Salmone			
GAM35	Hum	CAGCAGCA	ACTGCTGC	glg	NC_004631 f	lla e	3
3678	an	CACTGTGG	TC	P	rom 41292	nterica	--- -- ----- C
		TTTGTA			15 to 41316	ente	A C TGCTGCT A
					62 (+)	rica	T G ACGACGA
						serovar	ATG TT GTGTCAC C
				Typhi			
				Ty2			
GAM35	Hum	CAGCAGCA	AGAATGTT	rec	NC_002677 f	Mycobac	3
3678	an	CACTGTGG	GTTAGTGC	G	rom 20147	teriu m	--- -- T ITAG A
							AGA ATG TG

	TTTGTG	TGCTG	23 to 20169 54 (-)	leprae		TGCTGCTG	TTT TGT	
					AC	ACGACGAC	ATG GG	
					C	----		
GAM35	Hum	CAGCAGCA	rel NC_000962 f	Mycobac	3	---	AA AACTG	
3678	an	CACTGTGG	rom 29078	teriu m			AGACCATG G	A
		TTTGTG	24 to 29101	tubercu			GCTGCTG TTTGGTGT	
			96 (-)	los is	C		CGACGAC ATG	
				H3/Rv			CA ----A	
				Mycobac				
GAM35	Hum	CAGCAGCA	rel NC_002945 f	teriu m	3	---	AA AACTG	
3678	an	CACTGTGG	rom 28752	bovis			AGACCATG G	A
		TTTGTG	74 to 28776	subs p			GCTGCTG TTTGGTGT	
			46 (-)	bovis	C		CGACGAC ATG	
				AF21			CA ----A	
				22/97				
GAM35	Hum	CAGCAGCA	glp NC_003143 f	Yersini	3	---	- ----AG CT	A
3678	an	CACTGTGG	rom 42896	a pes			TGCTGCTG TT GG	
		TTTGTG	50 to 42908	tis			ACGACGAC ATG T	
			97 (-)				TGTCAC	
GAM35	Hum	CAGCAGCA	glp NC_004088 f	Yersini	3	---	- ----AG CT	A
3678	an	CACTGTGG	rom 4546	a pes			TGCTGCTG TT GG	
		TTTGTG	77 to 45604	tis KIM			ACGACGAC ATG T	
			7 (+)				TGTCAC	
GAM35	Hum	CAGCAGCA	fts NC_000922 f	Chlamyd	3	---	T A----G A	A
3678	an	CACTGTGG	rom 11154	ophila		ACCA	GCTGCTG T	A
		TTTGTG	27 to 11162	pneumon		TGGT	CGACGAC ATG T	
			99 (-)	iae			GTCACA	
				CWL029				
GAM35	Hum	CAGCAGCA	fts NC_002491 f	Chlamyd	3	---	T A----G A	A
3678	an	CACTGTGG	rom 11131	ophila		ACCA	GCTGCTG T	A
		TTTGTG	27 to 11139	pneumon		TGGT	CGACGAC ATG T	
			99 (-)	iae			GTCACA	
				J138				
GAM35	Hum	CAGCAGCA	SER		3	---	T ----A A	A
3678	an	CACTGTGG	PIN NM_001235	Human		ACCA	TG TGCTG T	
		TTTGTG	H 1			TGGT	AC ACGAC ATG T	
							GTCAC G	
				Leptosp				
GAM35	Hum	CAGCAGCA	aro NC_004342 f	nterrog	3	---	IT ----T	A
3678	an	CACTGTGG	rom 481	ans s		A TC	TGCTGCTG	
		TTTGTG	28 to 48832	erovar		T GG	ACGACGA	
			(-)	lai s		ATG TT	TGTCAC	C
				tr.				
				56601				
GAM35	Hum	CAGCAGCA	acc NC_002929 f	Bordete	3	--	A- C C	
3678	an	CACTGTGG	rom 9264	lla p		CAAA	ACGGT TGC GCTG	A
		TTTGTG	07 to 92777	ertussi		GTTT	TGTCAC ACG CGAC	
			7 (+)	s	AT	GS	C A	
GAM35	Hum	CAGCAGCA	zra NC_003197 f	Salmone	3	--	GC TITGCT	G
3678	an	CACTGTGG	rom 43877	lla t		CAAA	A T TGC	A
		TTTGTG	27 to 43881	yphimur		GCTG	GTTT T A	
			82 (-)	ium L			ACG CGAC AT	GG
				T2		GTC C----	A	
GAM35	Hum	CAGCAGCA	glp NC_004310 f	Brucell	3	--	GTGCTCTG	G
3678	an	CACTGTGG	rom 2107	a sui s		CAAA	A TGC	A
		TTTGTG	63 to 21227	1330		GCTG	GTTT T	
			4 (+)				ACG CGAC AT	
						GG	GTCAC----	A
GAM35	Hum	CAGCAGCA	avt NC_004337 f	Shigell	3	--	- G C- CAAAC	A
3678	an	CACTGTGG	rom 37211	a file		A G	TGCTGCTG GTTTG	
		TTTGTG	75 to 37225	xneri		T T	ACGACGAC AT	G

				33	(+)	2a str	G CAC	
						. 301		
						Shigell		
GAM35	Hum	CAGCAGCA	CAAAACAGG	avt	NC_004741	f a file	3	--
3678	an	CACTGTGG	CTGCTGCT	G A	rom 40526	xneri	A G	- G C-- CAAAC A
		TTTGTA			85 to 40539	2a str	T T	TCGTGCTG GTTTG G
					38 (-)	. 2457T	G CAC	
GAM35	Hum	CAGCAGCA	CAAAACATC	mia	NC_000117	f Chlamyd	3	--
3678	an	CACTGTGG	ATGGTTGC	A	rom 8992	ia tr	CAAAAC AT	- CA GT T
		TTTGTA	TGTTG		76 to 90029	achomat	TG	GTITG TG AC
					5 (+)	is	ACGAC AC AT	G TC
							--	G
GAM35	Hum	CAGCAGCA	CAAAACCAG	sel	NC_002947	f Pseudom	3	--
3678	an	CACTGTGG	CGGTCTGC	B	rom 5821	onas	CAAAACCA	G T CTGCTG A
		TTTGTA	TG		33 to 58405	putida	GTITGT	C A GACGAC
					5 (+)	KT244 0	AT	GT AC C
GAM35	Hum	CAGCAGCA	CAAAACCAT	mia	NC_000117	f Chlamyd	3	--
3678	an	CACTGTGG	GATGCTG	A	rom 8992	ia tr	CAAAACCA	TG TGCTG A
		TTTGTA			76 to 90029	achomat	GTITGT	AC ACGAC
					5 (+)	is	AT	GTAC G
GAM35	Hum	CAGCAGCA	CAAAACCGA	min	NC_002947	f Pseudom	3	--
3678	an	CACTGTGG	CCCTGCTG	E	rom 19326	onas	CAAAACCG	TGCTGCTG A
		TTTGTA	CTG		80 to 19329	putida	GTITGT	ACGACGAC
					34 (-)	KT244 0	AT	GTAC
GAM35	Hum	CAGCAGCA	CAAAACCGC	dna	NC_002677	f Mycobac	3	--
3678	an	CACTGTGG	AGTACTGG	E	rom 14230	teriu m	CAAAACCGCAGT	TG TGCTG A
		TTTGTA	TGCTG		14 to 14265	leprae	GTITGTGTGCA	AC ACGAC
					47 (+)		AT	C- G
						Leptosp		
						ira i		
GAM35	Hum	CAGCAGCA	CAAACTCT	aro	NC_004342	f nterrog	3	--
3678	an	CACTGTGG	TTTTCTTC	D	rom 481	ans s	CAAACT T T T	CTGCTG A
		TTTGTA	TGCTG		28 to 48832	erovar	GTITGG G A A	GACGAC
					(-)	lai s	AT	T TC C- C
						tr.		
						56601		
						Salmon		
GAM35	Hum	CAGCAGCA	CAAAAGCAC	pts	NC_003198	f nterica	3	--
3678	an	CACTGTGG	TGCTGCTG	H	rom 25084	ente	CAC	TGCTGCTG GTTT A
		TTTGTA			03 to 25056	rica	GTG	ACGACGAC AT G
					60 (+)	serovar	TCAC	
						Typhi		
GAM35	Hum	CAGCAGCA	CAAAAGCGG	amt	NC_004337	f Shigell	3	--
3678	an	CACTGTGG	CGTGCCTG	G B	rom 4080	a file	G CGC --	- A
		TTTGTA			59 to 40934	xneri	CAAA C G	TGC GCTG
					5 (+)	2a str	GTIT	G C ACG CGAC
						. 301	AT	G TGT AC A
GAM35	Hum	CAGCAGCA	CAAAAGCGG	amt	NC_004431	f Escheri	3	--
3678	an	CACTGTGG	CGTGCCTG	G B	rom 5476	chia	G CGC --	- A
		TTTGTA			16 to 54890	coli	CAAA C G	TGC GCTG
					2 (+)	CFT073	GTIT	G C ACG CGAC
							AT	G TGT AC A
						Shigell		
GAM35	Hum	CAGCAGCA	CAAAAGCGG	amt	NC_004741	f a file	3	--
3678	an	CACTGTGG	CGTGCCTG	G B	rom 4078	xneri	CAAA C G	TGC GCTG A
		TTTGTA			60 to 40914	2a str	GTIT	G C ACG CGAC
					6 (+)	. 2457T	AT	G TGT AC A
GAM35	Hum	CAGCAGCA	CAAAAGCCT	pil	NC_002947	f Pseudom	3	--
							G C	TT TTCG A

3678	an	CACTGTGG TTTGTA	TTTTTCGG GCTGCTG	T	rom 58169 34 to 58179 44 (-)	onas putida KT244 0	CAAA C T T GCTGCTG GTTT G G T TC C---A	
GAM35	Hum	CAGCAGCA	CAAAAGCGT	cys	NC_003197 f rom 25516	Salmone 3 lla t yphimur ium L T2	CAAA CGT TG TGCT A GCTG GTTT GTG AC ACGA CGAC AT G	
3678	an	CACTGTGG TTTGTA	CATGTAAT GCTTGCTG	M	51 to 25525 62 (-)		TC --- -	
GAM35	Hum	CAGCAGCA	CAAAATCCC	glc	NC_004431 f rom 35428	Escheri chia coli CFT073	- C CAGT - CAAATC CGT TG TGCTG A GTTTGG G AC ACACG	
3678	an	CACTGTGG TTTGTA	CAATTTGTC CTG	C	71 to 35436 95 (+)		AT T TCAC G	
GAM35	Hum	CAGCAGCA	CAACACAT	aro	NC_004337 f rom 15575	Shigell a file xnerl 2a str . 301	-- CA TACTGCT - CAA CAT TGCT A CTG GTT GTG ACGA GAC AT TG TCAC--- C	
3678	an	CACTGTGG TTTGTA	TACTGCTT GCTGCTG	H	27 to 15585 73 (-)			
GAM35	Hum	CAGCAGCA	CAACACTTT	spe	NC_003197 f rom 1942	Salmone 3 lla t yphimur ium L T2	-- - - TI-- - CAA C AC TGC GCTG A GTT G TG ACG CGAC	
3678	an	CACTGTGG TTTGTA	TGCGCTG	D	01 to 19499 5 (-)		AT T G TCAC A	
GAM35	Hum	CAGCAGCA	CAACACTTT	spe	NC_003198 f rom 1963	Salmone lla e nterica ente rica serovar Typhi	-- - - TI-- - CAA C AC TGC GCTG A GTT G TG ACG CGAC	
3678	an	CACTGTGG TTTGTA	TGCGCTG	D	89 to 19718 3 (-)		AT T G TCAC A	
GAM35	Hum	CAGCAGCA	CAACACTTT	spe	NC_004631 f rom 1963	Salmone lla e nterica 3 ente rica serovar Typhi Ty2	-- - - TI-- - CAA C AC TGC GCTG A GTT G TG ACG CGAC	
3678	an	CACTGTGG TTTGTA	TGCGCTG	D	80 to 19717 4 (-)		AT T G TCAC A	
GAM35	Hum	CAGCAGCA	CAACAGCA	ace	NC_002947 f rom 51847	Pseudom 3 onas putida KT244 0	-- - - GCAGT CAA C A TGCCTGCTG GTT G A T ACACGAC AT T G GTCAC	
3678	an	CACTGTGG TTTGTA	GTTGCTGC TG	K	42 to 51864 57 (-)			
GAM35	Hum	CAGCAGCA	CAACAGTT	fmt	NC_002745 f rom 22181	Staphyl ococc us 3 aureus su bsp. aureus N315	-- - - GTT CTGG - CAA C A T T A CTGCTG GTT G T A A GACGAC AT T G GTC C---- C	
3678	an	CACTGTGG TTTGTA	TCITGGTC TGCTG	B(m r p)	45 to 22255 90 (-)			
GAM35	Hum	CAGCAGCA	CAACAGTT	fmt	NC_002758 f rom 22879	Staphyl ococc us 3 aureus su bsp. aureus Mu50	-- - - GTT CTGG - CAA C A T T A CTGCTG GTT G T A A GACGAC AT T G GTC C---- C	
3678	an	CACTGTGG TTTGTA	TCITGGTC TGCTG	B(m r p)	35 to 22953 80 (-)			
GAM35	Hum	CAGCAGCA	CAACAGTT	tru	NC_003923 f rom 22380	Staphyl 3 ococc us aureus su bsp.	-- - - GTT CTGG - CAA C A T T A CTGCTG GTT G T A A GACGAC AT T G GTC C---- C	
3678	an	CACTGTGG TTTGTA	TCITGGTC TGCTG	nca t ed fmt	83 to 22401 43 (-)			

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GAM35	Hum	CAGCAGCA	CAAGCCTG	lpp	NC_000962	Myobac	3	--	-----	-	
3678	an	CACTGTGG	CGCTG	I	rom 22912	teriu m			CAAGCC	TGC GCTG	A
		TTTGTA			67 to 22919	tubercu			GTTTGG	ACG CGAC	
					23 (+)	los is			AT	TGTCAC	A
						H37Rv					
GAM35	Hum	CAGCAGCA	CAAGCCTG	lpp	NC_002945	Myobac	3	--	-----	-	
3678	an	CACTGTGG	CGCTG	I	rom 22751	teriu m			CAAGCC	TGC GCTG	A
		TTTGTA			82 to 22758	bovis			GTTTGG	ACG CGAC	
					38 (+)	subs p			AT	TGTCAC	A
						bovis					
						AF21					
						22/97					
GAM35	Hum	CAGCAGCA	CAAGCTGC	ris	NC_002929	Bordete	3	--	-----	CAAGC	A
3678	an	CACTGTGG	TGCTG	A	rom 37652	lla p			TGCTGCTG	GTTTG	
		TTTGTA			57 to 37659	ertussi			ACGACGAC	AT	
					91 (-)	s			GTGTAC		
GAM35	Hum	CAGCAGCA	CAAGGACC	acc	NC_002929	Bordete	3	--	GG	-----	-
3678	an	CACTGTGG	ATGCGCTG	C	rom 9264	lla p			GCTG	GTT TGGT	A
		TTTGTA			07 to 92777	ertussi			ACG CGAC	AT	--
					7 (+)	s			GTAC	A	
GAM35	Hum	CAGCAGCA	CAAGGCAA	xps	NC_002947	Pseudom	3	--	G A G	-	CAAG
3678	an	CACTGTGG	AGGTCTGC	T	rom 7070	onas			CA AG T	CTGCTG	GTTT
		TTTGTA			68 to 70734	putida			GT TC A	GACGAC	AT
					6 (-)	KT244 0			G AC C		G
GAM35	Hum	CAGCAGCA	CAATAACA	fmt	NC_002745	Staphyl	3	--	T A A	-----	A
3678	an	CACTGTGG	ATGCAGCT	B(m	rom 22181	ococc			CAA A CA	TGC GCTG	A
		TTTGTA		r	45 to 22255	us			GTT I GT	ACG CGAC	
				p)	90 (-)	aureus			AT	- G	GTCAC
						su bsp.					A
						aureus					
						N315					
GAM35	Hum	CAGCAGCA	CAATAACA	fmt	NC_002758	Staphyl	3	--	T A A	-----	A
3678	an	CACTGTGG	ATGCAGCT	B(m	rom 22879	ococc			CAA A CA	TGC GCTG	A
		TTTGTA		r	35 to 22953	us			GTT I GT	ACG CGAC	
				p)	80 (-)	aureus			AT	- G	GTCAC
						su bsp.					A
						aureus					
						Mu50					
GAM35	Hum	CAGCAGCA	CAATAACA	tru	NC_003923	Staphyl	3	--	T A A	-----	A
3678	an	CACTGTGG	ATGCAGCT	nca	rom 22380	ococc			CAA A CA	TGC GCTG	A
		TTTGTA		t	83 to 22401	us			GTT I GT	ACG CGAC	
				ed	43 (-)	aureus			AT	- G	GTCAC
				fmt		su bsp.					A
				B		aureus					
						MW2					
GAM35	Hum	CAGCAGCA	CAATAGCG	nup	NC_004337	Shigell	3	--	T-- GC CC	CAA	
3678	an	CACTGTGG	CCTGCTGC	C	rom 25158	a file			A G	TGCTGCTG	GTT
		TTTGTA			42 to 25170	xneri			T C	ACGACGAC	AT
					83 (+)	2a str			TGG GT	AC	
						. 301					
GAM35	Hum	CAGCAGCA	CAATAGCG	nup	NC_004431	Escheri	3	--	T-- GC CC	CAA	
3678	an	CACTGTGG	CCTGCTGC	C	rom 27953	chia			A G	TGCTGCTG	GTT
		TTTGTA			90 to 27966	coli			T C	ACGACGAC	AT
					31 (+)	CFT073			TGG GT	AC	
GAM35	Hum	CAGCAGCA	CAATAGCG	nup	NC_004741	Shigell	3	--	T-- GC CC	CAA	
3678	an	CACTGTGG	CCTGCTGC	C	rom 24940	a file			A G	TGCTGCTG	GTT
		TTTGTA			19 to 24952	xneri			T C	ACGACGAC	AT
					21 (+)	2a str			TGG GT	AC	
						. 2457T					

GAM35	Hum	CAGCAGCA	CAATATAG	NC_000922 f	Chlamy	3	--	TA	G AGC	A	A
3678	an	CACTGTGG	AAGCTGCT	def rom 12217	ophili a	3		CAA	TA A	TGCTGCT	
		TTTGTA	GCTA	35 to 12222	iae			GTT	GT T	ACGACGA	
				95 (+)	CWL029			AT	TG	G CAC	C
GAM35	Hum	CAGCAGCA	CAATATAG	NC_002491 f	Chlamy	3	--	TA	G AGC	A	A
3678	an	CACTGTGG	AAGCTGCT	def rom 12180	ophili a	3		CAA	TA A	TGCTGCT	
		TTTGTA	GCTA	69 to 12186	pneumon			GTT	GT T	ACGACGA	
				29 (+)	iae			AT	TG	G CAC	C
					J138						
GAM35	Hum	CAGCAGCA	CAATCACC	NC_004431 f	Escheri	3	--	T -	C G CCGA	G	
3678	an	CACTGTGG	GGGCCGAT	rom 35428	chia			CAA	C AC G G	TGC	A
		TTTGTA	GGGGCTG	71 to 35436	coli			GCTG	GTT G TG C C		
				95 (+)	CFT073			ACG	CGAC AT	T G T	
								A ----	A		
GAM35	Hum	CAGCAGCA	CAATCAGG	NC_002947 f	Pseudom	3	--	T -	G A- A	CAA	A
3678	an	CACTGTGG	GATACTGC	pta rom 8916	onas			C A	GG T	CTGCTG	GTT
		TTTGTA	TG	25 to 89371	putida			G T	TC A	GACGAC AT	T
				2 (-)	KT244 0			G G	AC C		
GAM35	Hum	CAGCAGCA	CAATCCCC	NC_002929 f	Bordete	3	--	T	C C - C	CAA	A
3678	an	CACTGTGG	GCTTCCTG	rom 12644	lla p			CC	CG T T	CTGCTG	GTT
		TTTGTA	CTG	36 to 12663	ertussi			GG	GT A A	GACGAC AT	T
				79 (+)	s			T	C C C		
GAM35	Hum	CAGCAGCA	CAATCCCG	NC_003143 f	Yersini	3	--	T	CG CCATT	-	
3678	an	CACTGTGG	GCCATTTC	rom 23364	a pes			CAA	CC G	TGCT	A
		TTTGTA	CTCTG	49 to 23374	tis			CTG	GTT GG T		
				53 (+)				ACGA	GAC AT	T TG	
								CAC--	C		
GAM35	Hum	CAGCAGCA	CAATCCCG	NC_004088 f	Yersini	3	--	T	CG CCATT	-	
3678	an	CACTGTGG	GCCATTTC	rom 24820	a pes			CAA	CC G	TGCT	A
		TTTGTA	CTCTG	31 to 24830	tis KIM			CTG	GTT GG T		
				35 (-)				ACGA	GAC AT	T TG	
								CAC--	C		
GAM35	Hum	CAGCAGCA	CAATCGCA	NC_004337 f	Shigell	3	--	T	G GCAC-	G	
3678	an	CACTGTGG	GCACGTGGT	rom 25158	a file			CAA	C CA	TG TGCTG	A
		TTTGTA	GCTG	42 to 25170	xneri			GTT	G GT	AC ACGAC	
				83 (+)	2a str			AT	T -	GTCAC	G
					. 301						
GAM35	Hum	CAGCAGCA	CAATCTCA	NC_002947 f	Pseudom	3	--	T T	IT C	-	
3678	an	CACTGTGG	CTTTCCTG	rom 7070	onas			CAA	C CAC	T TGC GCTG	A
		TTTGTA	GCTG	68 to 70734	putida			GTT	G GTG	A ACG CGAC	
				6 (-)	KT244 0			AT	T -	TC C	A
GAM35	Hum	CAGCAGCA	CACACAGG	NC_002677 f	Mycobac	3	--	C -	G TCACTCT	-	
3678	an	CACTGTGG	TCATCCTT	rom 15765	teriu m			CA	AC A G	TGC	A
		TTTGTA	GGCGTG	53 to 15773	leprae			GCTG	GT TG T T		
				50 (+)				ACG	CGAC AT	T G	
								G CAC----	A		
GAM35	Hum	CAGCAGCA	CACATGTT	NC_004337 f	Shigell	3	--	--	I TACA		
3678	an	CACTGTGG	GTACATGC	rom 25158	a file			I	CA C	ATG TG	A
		TTTGTA	TGCTT	42 to 25170	xneri			TGCTGCT	GI	G TGT	
				83 (+)	2a str			AC	ACGACGA	AT TT G	
					. 301			C ----	C		
GAM35	Hum	CAGCAGCA	CACCAATG	NC_000962 f	Mycobac	3	--	--	A----	C	A
3678	an	CACTGTGG	CTCCTG	rom 22912	teriu m			CA	CCA	TGCT CTG	A
		TTTGTA		67 to 22919	tubercu			GT	GGT	ACGA GAC	
				23 (+)	lor is			AT	TT	GTCAC	C
					H37Rv						
GAM35	Hum	CAGCAGCA	CACCAATG	NC_002945 f	Mycobac	3	--	--	A----	C	A
3678	an	CACTGTGG	CTCCTG	rom 22751	teriu m			CA	CCA	TGCT CTG	A
		TTTGTA		82 to 22758	bovis			GT	GGT	ACGA GAC	

				38	(+)	subs p	AT	TT	GTCAC	C	
						bovis					
						AF21					
						22/97					
GAM35	Hum	CAGCAGCA	CACCACCG	omp	NC_004431 f	Escheri	3	--	--	C CTAAC	
3678	an	CACTGTGG	CTAACTGC	G	rom 16245	chia			--	CA CCAC	G A
		TTTGTA	TGCG		77 to 16255	coli				TGCTGC G GT	GGTG
					33 (+)	CRT073		C		ACGACG C AT	TT
									T AC---	A	
						Salmone					
GAM35	Hum	CAGCAGCA	CACCACCT	phn	NC_003198 f	lla e	3	--	--	C--- C	CA A
3678	an	CACTGTGG	CCTGTCTG	V	rom 4715	nterica				T CTGTCTG	GT
		TTTGTA			75 to 47236	ente				CCAC	
					6 (-)	rica				GGTG	A GACGAC AT
						serovar			TT	TCAC C	
						Typhi					
						Salmone					
GAM35	Hum	CAGCAGCA	CACCACCT	phn	NC_004631 f	lla e	3	--	--	C--- C	CA A
3678	an	CACTGTGG	CCTGTCTG	V	rom 25087	nterica				T CTGTCTG	GT
		TTTGTA			35 to 25095	rica				GGTG	A GACGAC AT
					26 (+)	serovar			TT	TCAC C	
						Typhi					
						Ty2					
GAM35	Hum	CAGCAGCA	CACCACGT	pl1	NC_002947 f	Pseudom	3	--	--	TA	T
3678	an	CACTGTGG	AGTGTTC	T	rom 58169	onas			CA	CCACG	GTCT CTG
		TTTGTA	TG		34 to 58179	putida			GT	GGTG	CACGA GAC
					44 (-)	KT244 0		AT	TT	C	
						Salmone					
GAM35	Hum	CAGCAGCA	CACCACGG	oxy	NC_003197 f	lla t	3	--	--	GC CC	- CA A
3678	an	CACTGTGG	CCTGCGCT	G R	rom 43430	yphimur			CCA	G TGC	GCTG GT
		TTTGTA			80 to 43439	ium L			GGT	C ACG	CGAC AT
					97 (+)	T2			TT	GT AC	A
						Salmone					
GAM35	Hum	CAGCAGCA	CACCACGG	oxy	NC_003198 f	lla e	3	--	--	GC CC	- CA A
3678	an	CACTGTGG	CCTGCGCT	G R	rom 36072	nterica			CCA	G TGC	GCTG GT
		TTTGTA			04 to 36081	ente			GGT	C ACG	CGAC AT
					21 (-)	rica			TT	GT AC	A
						serovar					
						Typhi					
						Salmone					
GAM35	Hum	CAGCAGCA	CACCACGG	oxy	NC_004631 f	lla e	3	--	--	GC CC	- CA A
3678	an	CACTGTGG	CCTGCGCT	G R	rom 35928	nterica			CCA	G TGC	GCTG GT
		TTTGTA			64 to 35937	rica			GGT	C ACG	CGAC AT
					81 (-)	serovar			TT	GT AC	A
						Typhi					
						Ty2					
GAM35	Hum	CAGCAGCA	CACCATGC	MGA	NM_002410	Human	3	--	--	----- CA	
3678	an	CACTGTGG	TGCTG	T5					CCA	TGCTGCTG	GT A
		TTTGTA							GGT	ACGACGAC AT	
								TT	GTCAC		
						Shigell					
GAM35	Hum	CAGCAGCA	CACCATTTG	ipa	NC_004741 f	a file	3	--	--	----- C	
3678	an	CACTGTGG	CTGCCG	H_5	rom 20232	xneri			CA	CCAT	TGCTGC G
		TTTGTA			05 to 20248	2a str			GT	GGTG	ACGACG C
					48 (+)	. 2457T		AT	TT	TCAC	A
GAM35	Hum	CAGCAGCA	CACCATTTG	ipa	NC_004337 f	Shigell	3	--	--	----- C	
3678	an	CACTGTGG	CTGCCG	H9.	rom 14220	a file			CA	CCAT	TGCTGC G
		TTTGTA			8 64 to 14237	xneri			GT	GGTG	ACGACG C
					79 (-)	2a str		AT	TT	TCAC	A

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	TTTGTA	GTGCTG	60 to 14062	xneri	TGCTG	GI	IGGTGT	
			17 (-)	2a str		AC	ACGAC AT	T
				. 301		CAC---	G	
				Shigell				
GAM35 Hum	CAGCAGCA	CAGCCCAT	NC_004741 f	a file	3	--	C	TGTGTT -
3678 an	CACTGTGG	ATGTGTTT	rom 19046	xneri		CA	GCCATA	TG A
	TTTGTA	GTGCTG	66 to 19055	2a str		TGCTG	GI	IGGTGT
			23 (+)	. 2457T		AC	ACGAC AT	T
						CAC---	G	
GAM35 Hum	CAGCAGCA	CAGAACAC	NC_004337 f	Shigell	3	--	A	T TACC
3678 an	CACTGTGG	TGTTACCG	rom 39477	a file		CAGA	CAC GT	T
	TTTGTA	CTGCTG	08 to 39487	xneri		GTGCTG	GTTT	GIG
			00 (+)	. 301		CA	CGACGAC AT	G
						T	C--A	
GAM35 Hum	CAGCAGCA	CAGAACAC	NC_004431 f	Escheri	3	--	A	T TACC
3678 an	CACTGTGG	TGTTACCG	rom 44392	chia		CAGA	CAC GT	T
	TTTGTA	CTGCTG	60 to 44402	coli		GTGCTG	GTTT	GIG
			52 (+)	CTF073		CA	CGACGAC AT	G
						T	C--A	
GAM35 Hum	CAGCAGCA	CAGAACAC	NC_004741 f	Shigell	3	--	A	T TACC
3678 an	CACTGTGG	TGTTACCG	rom 38245	xneri		CAGA	CAC GT	T
	TTTGTA	CTGCTG	94 to 38255	2a str		GTGCTG	GTTT	GIG
			77 (-)	. 2457T		CA	CGACGAC AT	G
						T	C--A	
GAM35 Hum	CAGCAGCA	CAGAAGCA	NC_004337 f	Shigell	3	--	G	G AACAT CA
3678 an	CACTGTGG	TGAACATT	rom 39477	a file		AA	CATG	TGCTGCTG
	TTTGTA	GCTGCTG	08 to 39487	xneri		GT	TT GTGT	
			00 (+)	. 301		ACGACGAC	AT -	G
						CAC--		
GAM35 Hum	CAGCAGCA	CAGAAGCA	NC_004741 f	Shigell	3	--	G	G AACAT CA
3678 an	CACTGTGG	TGAACATT	rom 38245	xneri		AA	CATG	TGCTGCTG
	TTTGTA	GCTGCTG	94 to 38255	2a str		GT	TT GTGT	
			77 (-)	. 2457T		ACGACGAC	AT -	G
						CAC--		
GAM35 Hum	CAGCAGCA	CAGACGAT	NC_002516 f	Pseudom	3	--	G	C--- C
3678 an	CACTGTGG	CTCCTGCT	rom 46535	onas		CAGAC	AT	TIGCTGT
	TTTGTA		08 to 46543	aerugin		GTTTG	TG	A CACGAC
			05 (-)	osa P		AT	G	TCAC C
				A01				
GAM35 Hum	CAGCAGCA	CAGACTCA	NC_002947 f	Pseudom	3	--	T	GC--- C
3678 an	CACTGTGG	GCTGTGTC	rom 58169	onas		CAGAC	CA	TGCTGCT
	TTTGTA	TC	34 to 58179	putida		GTTTG	GT	ACGACGA
			44 (-)	KT244 0		AT	-	GTAC C
GAM35 Hum	CAGCAGCA	CAGCAGGC	NC_003198 f	Salmone	3	--	-	G C T CAG C
3678 an	CACTGTGG	TTTGTGTC	rom 45373	nterica		A	G T	TGCTGCTG
	TTTGTA	IG	12 to 45375	ente		T	T A	ACGACGAC AT
			33 (+)	rica		G	C C	T G
				serovar				
				Typhi				
GAM35 Hum	CAGCAGCA	CAGCAGGC	NC_004631 f	Salmone	3	--	-	G C T CAG C
3678 an	CACTGTGG	TTTGTGTC	rom 45201	nterica		A	G T	TGCTGCTG
	TTTGTA	IG	21 to 45203	ente		T	T A	ACGACGAC AT
			42 (+)	rica		G	C C	T G
				serovar				
				Typhi				
				Ty2				
GAM35 Hum	CAGCAGCA	CAGCCACA	NC_002947 f	Pseudom	3	--	-	----A CAG A
3678 an	CACTGTGG	GCTGCTG	rom 48716	onas		CCAC	GCTGCTG	GTT

		TTTGTGA		25 to 48729 29 (+)	putida KT244 0	GGTG TCACA	CGACGAC AT T	
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTGA	CAGCCAGG TTTTGCTC TG	phn V	NC_003198 f rom 4715 75 to 47236 6 (-)	Salmone lla e nterica ente rica serovar Typhi Salmone lla e nterica ente rica serovar Typhi Ty2	3 -- - G I T - CAG CCA G T TGCT CTG GTT GGT T A ACGA GAC AT T G C C C	A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTGA	CAGCCAGG TTTTGCTC TG	phn V	NC_004631 f rom 25087 35 to 25095 26 (+)	Salmone lla e nterica ente rica serovar Typhi Ty2	3 -- - G I T - CAG CCA G T TGCT CTG GTT GGT T A ACGA GAC AT T G C C C	A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTGA	CAGCGAGG CCTGCTGC TGCTG	tcf A	NC_002929 f rom 12644 36 to 12663 79 (+)	Bordete lla p ertussi s	3 -- - G G CCICG CAG C A G TGCTGCTG GTT G T T ACGACGAC AT T G G CAC--	A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTGA	CAGCGCTT GGGTGATC TGCTG	uhp A	NC_003143 f rom 45227 90 to 45233 80 (-)	Yersini a pes tis	3 -- CG T A CAG C TGGTG TGCTGCTG G GTAC ACGACGAC AT TG T -	A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTGA	CAGGCGCA GGGTGCTG TGCTG	cys Q	NC_002947 f rom 3151 84 to 31598 4 (+)	Pseudom onas putida KT244 0	3 -- G G CAGG CA GGTGTGCTGCTG GTTG GT TCACACGACGAC AT - G	A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTGA	CATACCTC CCGCACTG CTGCCG	pbp G	NC_002947 f rom 43237 07 to 43246 33 (+)	Pseudom onas putida KT244 0	3 -- T T CCGCAC C CA ACC C TGCTGC A G GT TGG G ACGACG C AT T T TCAC-- A	A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTGA	CATACTG CTGCTG	ung	NC_000907 f rom 186 76 to 19335 (+)	Haemoph ilus influen zae R d	3 -- T ----- CA ATC TGCTGCTG GT TGG ACGACGAC AT T TGTCAC	A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTGA	CATCCACA CGCTGCTG	ssb	NC_002947 f rom 5710 27 to 57157 2 (+)	Pseudom onas putida KT244 0	3 -- T- ---C CA CCACA GCTGCTG GT GGTGT CAGACGAC AT TT CACA	A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTGA	CATCCATA TCGCCATT GCTGCTG	rbs R	NC_004431 f rom 44392 60 to 44402 52 (+)	Escheri chia coli CFT073	3 -- T- TC CCAT G CA CCATA G TGCTG TG GT GGTGT C ACGAC AC AT TT CA ---- G	A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTGA	CATCCCGG GCCGCTG CTGCTC	glp C	NC_003143 f rom 42896 50 to 42908 97 (-)	Yersini a pes tis	3 -- TCG G CGGCG C CA CG G TGCTGCT GT GT T ACGACG A AT TT G CAC-- C	A
GAM35 3678	Hum an	CAGCAGCA CACTGTGG TTTGTGA	CATCCCGG GCCGCTG CTGCTC	glp C	NC_004088 f rom 4546 77 to 45604 7 (+)	Yersini a pes tis KIM	3 -- TCG G CGGCG C CA CG G TGCTGCT GT GT T ACGACG A AT TT G CAC-- C	A
GAM35	Hum	CAGCAGCA	CATGTCGG	dna	NC_002677 f	Mycobac	3 -- T GT GIGGA	A

3678	an	CACTGTGG TTTGTA	TGGTGGAT GCTGCTT	E	rom 14230 14 to 14265 47 (+)	teriu m leprae	T CA GTGG G TGCTGCT GT TGGT ACGACGA AT T GT AC---	
GAM35	Hum	CAGCAGCA	CATGTGCG	pcn	NC_002677 f rom 32482	Mycobac 3 teriu m	T GT GIGGA CA GTGG G	A
3678	an	CACTGTGG TTTGTA	TGGTGGAT GCTGCTT	A	68 to 32497 28 (-)	leprae	TGCTGCT GT TGGT ACGACGA AT T GT AC---	
GAM35	Hum	CAGCAGCA	CATGTGCG	pol	NC_002677 f rom 16482	Mycobac 3 teriu m	T GT GIGGG CA GTGG G	A
3678	an	CACTGTGG TTTGTA	TGGTGGAT GCTGCTT	A	20 to 16509 55 (-)	leprae	TGCTGCT GT TGGT ACGACGA AT T GT AC---	
GAM35	Hum	CAGCAGCA	CATGTGCG	tru	NC_002677 f rom 23433	Mycobac 3 teriu m	T GT GIGGG CA GTGG G	A
3678	an	CACTGTGG TTTGTA	TGGTGGAT GCTGCTT	A	29 to 23440 78 (-)	leprae	TGCTGCT GT TGGT ACGACGA AT T GT AC---	
GAM35	Hum	CAGCAGCA	CCCGTGCT	omp	NC_004431 f rom 16245	Escheri chia	T C CGG TGCTGCT	A
3678	an	CACTGTGG TTTGTA	GCTT	G	77 to 16255 33 (+)	coli CFT073	G TGTGCT AT TGT GTCAC	
GAM35	Hum	CAGCAGCA	CCCTCGGT	flh	NC_002929 f rom 14417	Bordete 3 lla p	T -- C CC CGG TGCTGCTG G GG	A
3678	an	CACTGTGG TTTGTA	GCTGCTG	B	67 to 14429 21 (+)	ertussi s	GTC ACGACGAC AT TTT T AC	
GAM35	Hum	CAGCAGCA	CGAACACC	aer	NC_002947 f rom 24069	Pseudom onas	C A- CGAACACC G TGCTG TG	A
3678	an	CACTGTGG TTTGTA	GATGCTG TG	-2	96 to 24085 61 (-)	putida KT244 0	GTITGGTG C ACGAC AT T AC G	
GAM35	Hum	CAGCAGCA	CGAACGTG	prc	NC_002677 f rom 15765	Mycobac 3 teriu m	G----- CGAAC TGCTGCTG GTTG	A
3678	an	CACTGTGG TTTGTA	CTGCTG	A	53 to 15773 50 (+)	leprae	ACGACGAC AT GTGTCAC	
GAM35	Hum	CAGCAGCA	CGACACC	van	NC_002516 f rom 55041	Pseudom onas	-- - C C G CGA CCAC G GTG TGCTG GTT	A
3678	an	CACTGTGG TTTGTA	GCTGTGGT CTG	B	20 to 55050 73 (+)	aerugin osa P A01	GGTG C CAC ACGAC AT T T A G	
GAM35	Hum	CAGCAGCA	CGACTGCT	pch	NC_002516 f rom 47451	Pseudom onas	-- - - - - CGA C TGCTGCTG GTT G	A
3678	an	CACTGTGG TTTGTA	GCTG	A	20 to 47465 50 (+)	aerugin osa P A01	ACGACGAC AT T GTGTCAC	
GAM35	Hum	CAGCAGCA	CGAGCGAT	dsd	NC_003197 f rom 40044	Salmone lla t	-- G ----- T CGAGC A TGCTGCT	A
3678	an	CACTGTGG TTTGTA	GCTGCTT	A	53 to 40057 75 (+)	yphimur ium L T2	GTITG T ACGACGA AT G GTCAC	
GAM35	Hum	CAGCAGCA	CGAGGGAT	nic	NC_000962 f rom 31666	Mycobac teriu m	-- GG TA C CGAG ATG GTGCTGCT	A
3678	an	CACTGTGG TTTGTA	GTAGTGCT GCTC	T	81 to 31677 99 (+)	tubercu los is H37Rv	GTIT TGT CACGACGA AT GG CA C	
GAM35	Hum	CAGCAGCA	CGAGGGAT	nic	NC_002945 f rom 31232	Mycobac teriu m	-- GG TA C CGAG ATG GTGCTGCT	A
3678	an	CACTGTGG TTTGTA	GTAGTGCT GCTC	T	00 to 31243 18 (+)	bovis subs p bovis AF21	GTIT TGT CACGACGA AT GG CA C	

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GAM35	Hum	CAGCAGCA	CGCCAGAT	yab	NC_004431 f	Escheri	3	--	--	G T--	CG	A
3678	an	CACTGTGG	TGCTGCTG	O	rom 614	chia				CCA A	TGCTGCTG	GT
		TTTGTA			89 to 62148	coli				GGT T	ACGACGAC	AT
					(-)	CFT073				TT	G CAC	
GAM35	Hum	CAGCAGCA	CGCCGGTT	pch	NC_002516 f	Pseudom	3	--	--	GT---	CG	A
3678	an	CACTGTGG	GCTGCTG	A	rom 47451	onas				CCG	TGCTGCTG	GT
		TTTGTA			20 to 47465	aerugin				GGT	ACGACGAC	AT
					50 (+)	osa P				TT	GTACAC	
						A01						
GAM35	Hum	CAGCAGCA	CGCCGGTT	fep	NC_002516 f	Pseudom	3	--	--	GT---	T	A
3678	an	CACTGTGG	GCTGCTT	C	rom 46535	onas				CG	TGCTGCTG	GT
		TTTGTA			08 to 46543	aerugin				GT	GGT	ACGACGAC
					05 (-)	osa P				AT	TT	GTACAC
						A01						
GAM35	Hum	CAGCAGCA	CGCTGCTG	liv	NC_002929 f	Bordete	3	--	--	-----	CG	C
3678	an	CACTGTGG	CTG	H	rom 11447	lla p				TGCTGCTG	GT	T
		TTTGTA			29 to 11456	ertussi				ACGACGAC	AT	TT
					07 (+)	s				GTGTACAC		
GAM35	Hum	CAGCAGCA	CGGAATTT	ycl	NC_004431 f	Escheri	3	--	--	T---	CGGA	A
3678	an	CACTGTGG	GCTGCTG	E	rom 15586	chia				AT	TGCTGCTG	GT
		TTTGTA			41 to 15591	coli				TT	ACGACGAC	AT
					47 (-)	CFT073				GG	TCAC	
GAM35	Hum	CAGCAGCA	CGTCCACG	flh	NC_002929 f	Bordete	3	--	T-	CG	GTTG	
3678	an	CACTGTGG	CGGGTGGT	B	rom 14417	lla p				C	CG	CCACG
		TTTGTA			67 to 14429	ertussi				TGCTGCT	GT	GGTGT
					21 (+)	s				C	ACGACGAC	AT
										CA	----	C
GAM35	Hum	CAGCAGCA	CGTCCATC	pbp	NC_002947 f	Pseudom	3	--	T-	CT--	C	A
3678	an	CACTGTGG	TTGCTGCT	G	rom 43237	onas				CG	CCAT	TGCTGCT
		TTTGTA			07 to 43246	putida				GT	GGT	ACGACGAC
					33 (+)	KT244 0				AT	TT	TCAC
GAM35	Hum	CAGCAGCA	CGTCTGTC	aco	NC_002516 f	Pseudom	3	--	T-	-----	CG	CC
3678	an	CACTGTGG	TGCTG	R	rom 46395	onas				TGCTGCTG	GT	GG
		TTTGTA			01 to 46413	aerugin				ACGACGAC	AT	TT
					78 (-)	osa P				GTGTACAC		
						A01						
GAM35	Hum	CAGCAGCA	CGTGCCTG	ace	NC_002947 f	Pseudom	3	--	T	-----	C	A
3678	an	CACTGTGG	CTGCTC	K	rom 51847	onas				CG	GCC	TGCTGCT
		TTTGTA			42 to 51864	putida				GT	TGG	ACGACGAC
					57 (-)	KT244 0				AT	T	GTGTAC
GAM35	Hum	CAGCAGCA	CTAAAGTG	rec	NC_002677 f	Mycobac	3	--	T	G----	C	AA
3678	an	CACTGTGG	CTGCTG	G	rom 20147	teriu m				A	TGCTGCTG	G
		TTTGTA			23 to 20169	leprae				T	ACGACGAC	AT
					54 (-)					GG	GTACAC	
GAM35	Hum	CAGCAGCA	CTAACACG	ung	NC_000907 f	Haemoph	3	--	T	-	CGC	-
3678	an	CACTGTGG	CGCTGCTC		rom 186	ilus				AAC	ACG	TGCT
		TTTGTA			76 to 19335	influen				TTG	TGT	ACGA
					(+)	zae R d				G	CAC	C
GAM35	Hum	CAGCAGCA	CTAACCTG	cII	NC_003198 f	Salmone	3	--	T	TGTA--	-	C
3678	an	CACTGTGG	TATCTGCT	G	rom 45373	lla e				AAAC	T	CTGCTG
		TTTGTA			12 to 45375	nterica				TTGG	A	GACGAC
					33 (+)	ente						AT
						rica						TT
						serovar						
						Typhi						
GAM35	Hum	CAGCAGCA	CTAACCTG	cII	NC_004631 f	Salmone	3	--	T	TGTA--	-	C

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3678 an CACTGTGG TATCTGCT G rom 45201 lla e AACC T CTGCTG G
      TTTGTA 21 to 45203 nterica TTGG A GACGAC AT T
      42 (+) ente TGTACAC C
      rica
      serovar
      Typhi
      Ty2

GAM35 Hum CAGCAGCA CTACCTGC uhp NC_003143 f Yersini 3 -- T - TGCC-- C A CC
3678 an CACTGTGG CTGCTGCT G A rom 45227 a pes TGCTGCTG G T GG A
      TTTGTA 90 to 45233 tis ACACGAC AT T T
      80 (-) TGTACAC

GAM35 Hum CAGCAGCA CTAGCCCT aco NC_002516 f Pseudom 3 -- T C----- C
3678 an CACTGTGG GCTGCTC R rom 46395 onas C AGCC TGCTGCT C A
      TTTGTA 01 to 46413 aerugin C TTGG ACACGAC C
      78 (-) A01 AT T TGTACAC C

GAM35 Hum CAGCAGCA CTGCTGCT ssb NC_002947 f Pseudom 3 -- T-- ----- C CC
3678 an CACTGTGG GCTG rom 5710 onas TGCTGCTG G GG A
      TTTGTA 27 to 57157 putida ACACGAC AT TTT
      2 (+) KT244 0 TGTACAC

GAM35 Hum CAGCAGCA CTGGGGTT fha NC_002929 f Bordete 3 -- T-- G GTI CT C C
3678 an CACTGTGG TCTGCTG L rom 30858 lla p G T TGCTGCTG G C
      TTTGTA CTG 65 to 30984 ertussi T A ACACGAC AT TTT
      55 (+) s G GTC C-

GAM35 Hum CAGCAGCA CTGACCTT pta NC_002947 f Pseudom 3 -- T T----- C
3678 an CACTGTGG GCTGCTC rom 8916 onas C GACC TGCTGCT C A
      TTTGTA 25 to 89371 putida G TTGG ACACGAC C
      2 (-) KT244 0 AT T TGTACAC C

GAM35 Hum CAGCAGCA CTGCCTGC orn NC_003143 f Yersini 3 -- T - ----- C
3678 an CACTGTGG TGCTC rom 3783 a pes C G CC TGCTGCT C A
      TTTGTA 31 to 37887 tis C T GG ACACGAC C
      6 (+) AT T T TGTACAC C

GAM35 Hum CAGCAGCA CTGCGTGC glp NC_004310 f Brucell 3 -- T - G----- T
3678 an CACTGTGG TGCTT D rom 2107 a sui s C G C TGCTGCT T A
      TTTGTA 63 to 21227 1330 G T G ACACGAC C
      4 (+) AT T T TGTCAC C

GAM35 Hum CAGCAGCA CTTACTTG sse NC_004431 f Escheri 3 -- TT ----- C
3678 an CACTGTGG CTGCTC B rom 29224 chia C ACT TGCTGCT C A
      TTTGTA 56 to 29232 coli G TGG ACACGAC C
      41 (-) CFT073 AT TT TGTACAC C

GAM35 Hum CAGCAGCA CTTCCTGC def NC_000922 f Chlamyd 3 -- TT- ----- T
3678 an CACTGTGG TGCTT rom 12217 pneumon C CC TGCTGCT T A
      TTTGTA 35 to 12222 iae G GG ACACGAC C
      95 (+) CWL029 AT TTT TGTACAC C

GAM35 Hum CAGCAGCA CTTCCTGC def NC_002491 f Chlamyd 3 -- TT- ----- T
3678 an CACTGTGG TGCTT rom 12180 ophil a C CC TGCTGCT T A
      TTTGTA 69 to 12186 pneumon G GG ACACGAC C
      29 (+) iae AT TTT TGTACAC C
      J138

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Replace paragraph 0159 with the following paragraph.

It is appreciated that the specific functions and accordingly the utilities of each of a plurality of GAM oligonucleotides that are described by Fig. 1 are correlated with and may be deduced from the

identity of the GAM TARGET GENES inhibited thereby, and whose functions are set forth in Table 8, hereby incorporated herein. Table 8, lines 685695-687709 shows data relating to the function and utilities of GAM RNA as set forth in SEQ ID NO: 348.

After paragraph 0159, add the following Table 8.

Table 8

GAM NAME	GAM RNA SEQUENCE	GAM ORGANISM	TARGET GET	TARGET ORGANISM	GAM FUNCTION	GAM POS
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	acc cC	Bordetella pertussis	GAM353678 is a human miRNA-like oligonucleotide, which targets biotin carboxylase (accC, NC_002929 from 926407 to 927777 (+)), a bacterial target gene encoded by the Bordetella pertussis genome, as part of an anti-bacterial host defense mechanism. accC BINDING SITE 1 and accC BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the accC gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of accC BINDING SITE 1 and accC BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. A function of GAM353678 is to inhibit accC, a GAM353678 bacterial target gene which is associated with Bordetella pertussis infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Bordetella pertussis infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	acc eK	Pseudomonas putida KT2440	GAM353678 is a human miRNA-like oligonucleotide, which targets isocitrate dehydrogenase kinase/phosphatase (aceK, NC_002947 from 5184742 to 5186457 (-)), a bacterial target gene encoded by the Pseudomonas putida KT2440 genome, as part of an anti-bacterial host defense mechanism. aceK BINDING SITE 1 and aceK BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the aceK gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of aceK BINDING SITE 1 and aceK BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit aceK, a GAM353678 bacterial target gene which is associated with Pseudomonas putida KT2440 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of	A

GAM353678 CAGCAGCA CACTGTGG TTTGTA	Human	acoR Pseudomonas aeruginosa PAO1	<p>GAM353678 include the diagnosis, prevention and treatment of <i>Pseudomonas putida</i> KT2440 infection and associated clinical conditions</p> <p>GAM353678 is a human miRNA-like oligonucleotide, which targets transcriptional regulator AcoR (acoR, NC_002516 from 4639501 to 4641378 (-)), a bacterial target gene encoded by the <i>Pseudomonas aeruginosa</i> PAO1 genome, as part of an anti-bacterial host defense mechanism. acoR BINDING SITE 1 and acoR BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the acoR gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of acoR BINDING SITE 1 and acoR BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit acoR, a GAM353678 bacterial target gene which is associated with <i>Pseudomonas aeruginosa</i> PAO1 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Pseudomonas aeruginosa</i> PAO1 infection and associated clinical conditions</p>	A
GAM353678 CAGCAGCA CACTGTGG TTTGTA	Human	aer-2 Pseudomonas putida KT2440	<p>GAM353678 is a human miRNA-like oligonucleotide, which targets aerotaxis receptor Aer-2 (aer-2, NC_002947 from 2406996 to 2408561 (-)), a bacterial target gene encoded by the <i>Pseudomonas putida</i> KT2440 genome, as part of an anti-bacterial host defense mechanism. aer-2 BINDING SITE 1 and aer-2 BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the aer-2 gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of aer-2 BINDING SITE 1 and aer-2 BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit aer-2, a GAM353678 bacterial target gene which is associated with <i>Pseudomonas putida</i> KT2440 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Pseudomonas putida</i> KT2440 infection and associated clinical conditions</p>	A
GAM353678 CAGCAGCA CACTGTGG TTTGTA	Human	amtB Shigella flexneri 2a str. 301	<p>GAM353678 is a human miRNA-like oligonucleotide, which targets probable ammonium transporter (amtB, NC_004337 from 408059 to 409345 (+)), a bacterial target gene encoded by the <i>Shigella flexneri</i> 2a str. 301 genome, as part of an anti-bacterial host defense mechanism. amtB BINDING SITE 1 and amtB BINDING SITE</p>	A

					2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the <i>amtB</i> gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of <i>amtB</i> BINDING SITE 1 and <i>amtB</i> BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit <i>amtB</i> , a GAM353678 bacterial target gene which is associated with <i>Shigella flexneri</i> 2a str. 301 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Shigella flexneri</i> 2a str. 301 infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTGA	Human	<i>amtB</i>	<i>Escherichia coli</i> CFT073	GAM353678 is a human miRNA-like oligonucleotide, which targets Probable ammonium transporter (<i>amtB</i> , NC_004431 from 547616 to 548902 (+)), a bacterial target gene encoded by the <i>Escherichia coli</i> CFT073 genome, as part of an anti-bacterial host defense mechanism. <i>amtB</i> BINDING SITE 1 and <i>amtB</i> BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the <i>amtB</i> gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of <i>amtB</i> BINDING SITE 1 and <i>amtB</i> BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit <i>amtB</i> , a GAM353678 bacterial target gene which is associated with <i>Escherichia coli</i> CFT073 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Escherichia coli</i> CFT073 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTGA	Human	<i>amtB</i>	<i>Shigella flexneri</i> 2a str. 2457T	GAM353678 is a human miRNA-like oligonucleotide, which targets Probable ammonium transporter (<i>amtB</i> , NC_004741 from 407860 to 409146 (+)), a bacterial target gene encoded by the <i>Shigella flexneri</i> 2a str. 2457T genome, as part of an anti-bacterial host defense mechanism. <i>amtB</i> BINDING SITE 1 and <i>amtB</i> BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the <i>amtB</i> gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of <i>amtB</i> BINDING SITE 1 and <i>amtB</i> BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit <i>amtB</i> , a GAM353678	A

					bacterial target gene which is associated with <i>Shigella flexneri</i> 2a str. 2457T infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Shigella flexneri</i> 2a str. 2457T infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	aroA	<i>Neisseria meningitidis</i> Z2491	GAM353678 is a human miRNA-like oligonucleotide, which targets 5'-enolpyruvylshikimate-3-phosphate synthase (aroA, NC_003116 from 1557502 to 1558803 (+)), a bacterial target gene encoded by the <i>Neisseria meningitidis</i> Z2491 genome, as part of an anti-bacterial host defense mechanism. aroA BINDING SITE 1 and aroA BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the aroA gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of aroA BINDING SITE 1 and aroA BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit aroA, a GAM353678 bacterial target gene which is associated with <i>Neisseria meningitidis</i> Z2491 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Neisseria meningitidis</i> Z2491 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	aroD	<i>Leptospira interrogans</i> serovar lai str. 56601	GAM353678 is a human miRNA-like oligonucleotide, which targets 3'-dehydroquinate dehydratase (aroD, NC_004342 from 48128 to 48832 (-)), a bacterial target gene encoded by the <i>Leptospira interrogans</i> serovar lai str. 56601 genome, as part of an anti-bacterial host defense mechanism. aroD BINDING SITE 1 and aroD BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the aroD gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of aroD BINDING SITE 1 and aroD BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit aroD, a GAM353678 bacterial target gene which is associated with <i>Leptospira interrogans</i> serovar lai str. 56601 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Leptospira interrogans</i> serovar lai str. 56601 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	aroH	<i>Shigella flexneri</i> 2a str. 3	GAM353678 is a human miRNA-like oligonucleotide, which targets 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	A

01					(DAHPh synthetase, tryptophan repressible) (aroH, NC_004337 from 15575 to 1558573 (-)), a bacterial target gene encoded by the <i>Shigella flexneri</i> 2a str. 301 genome, as part of an anti-bacterial host defense mechanism. aroH BINDING SITE 1 and aroH BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the aroH gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of aroH BINDING SITE 1 and aroH BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit aroH, a GAM353678 bacterial target gene which is associated with <i>Shigella flexneri</i> 2a str. 301 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Shigella flexneri</i> 2a str. 301 infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	avtA	<i>Shigella flexneri</i> 2a str. 301	GAM353678 is a human miRNA-like oligonucleotide, which targets alanine- α -ketoisovalerate (or valine-pyruvate) transaminase C (avtA, NC_004337 from 3721175 to 3722533 (+)), a bacterial target gene encoded by the <i>Shigella flexneri</i> 2a str. 301 genome, as part of an anti-bacterial host defense mechanism. avtA BINDING SITE is a bacterial target binding site that is a found in the the 3' untranslated region of mRNA encoded by the avtA gene, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of avtA BINDING SITE, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit avtA, a GAM353678 bacterial target gene which is associated with <i>Shigella flexneri</i> 2a str. 301 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Shigella flexneri</i> 2a str. 301 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	avtA	<i>Shigella flexneri</i> 2a str. 2457T	GAM353678 is a human miRNA-like oligonucleotide, which targets alanine- α -ketoisovalerate/valine-pyruvate transaminase C (avtA, NC_004741 from 4052685 to 4053938 (-)), a bacterial target gene encoded by the <i>Shigella flexneri</i> 2a str. 2457T genome, as part of an anti-bacterial host defense mechanism. avtA BINDING SITE is a bacterial target binding site that is a found in the the 3' untranslated region of mRNA encoded by the avtA gene, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of	A

GAM353678 CAGCAGCA CACTGTGG TTTGTG	Human cII Salmonella enterica enterica serovar Typhi Ty2	GAM353678 is a human miRNA-like oligonucleotide, which targets transcriptional regulatory protein (cII, NC_004631 from 452 0121 to 4520342 (+)), a bacterial target gene encoded by the Salmonella enterica enterica serovar Typhi Ty2 genome, as part of an anti-bacterial host defense mechanism. cII BINDING SITE 1 and cII BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the cII gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE I II of Fig. 1. The nucleotide sequences of cII BINDING SITE 1 and cII BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit cII, a bacterial target gene which is associated with Salmonella enterica enterica serovar Typhi Ty2 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Salmonella enterica enterica serovar Typhi Ty2 infection and associated clinical conditions	A
GAM353678 CAGCAGCA CACTGTGG TTTGTG	Human cII Salmonella enterica enterica serovar Typhi	GAM353678 is a human miRNA-like oligonucleotide, which targets transcriptional regulatory protein (cII, NC_003198 from 453 7312 to 4537533 (+)), a bacterial target gene encoded by the Salmonella enterica enterica serovar Typhi genome, as part of an anti-bacterial host defense mechanism. cII BINDING SITE 1 and cII BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the cII gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE I II of Fig. 1. The nucleotide sequences of cII BINDING SITE 1 and cII BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit cII, a bacterial target gene which is associated with Salmonella enterica enterica serovar Typhi infection, as part of an anti-bacterial host defense mechanism. Accordingly,	A

GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	cysM	Salmonella typhimurium LT2	the utilities of GAM 353678 include the diagnosis, prevention and treatment of Salmonella enterica enterovar Typhi infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	cysQ	Pseudomonas putida KT2440	GAM353678 is a human miRNA-like oligonucleotide, which targets cysteine synthase B (cysM, NC_003197 from 2551651 to 2552562 (-)), a bacterial target gene encoded by the Salmonella typhimurium LT2 genome, as part of an anti-bacterial host defense mechanism. cysM BINDING SITE 1 and cysM BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the cysM gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of cysM BINDING SITE 1 and cysM BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit cysM, a GAM353678 bacterial target gene which is associated with Salmonella typhimurium LT2 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Salmonella typhimurium LT2 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	dadX	Escherichia coli CFT073	GAM353678 is a human miRNA-like oligonucleotide, which targets 3'(2'),5'-bisphosphate nucleotidase (cysQ, NC_002947 from 315184 to 315984 (+)), a bacterial target gene encoded by the Pseudomonas putida KT2440 genome, as part of an anti-bacterial host defense mechanism. cysQ BINDING SITE 1 and cysQ BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the cysQ gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of cysQ BINDING SITE 1 and cysQ BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit cysQ, a GAM353678 bacterial target gene which is associated with Pseudomonas putida KT2440 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Pseudomonas putida KT2440 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	dadX	Escherichia coli CFT073	GAM353678 is a human miRNA-like oligonucleotide, which targets Alanine racemase, catabolic (dadX, NC_004431 from 1476306 to 1477376 (+)), a bacterial target gene encoded by the Escherichia coli CFT073 genome, as part of an anti-bacterial host defense mechanism. dadX BINDING SITE 1 and dadX BINDING SITE 2 are bacterial target binding sites that are	A

					found in the untranslated regions of mRNA encoded by the dadX gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of dadX BINDING SITE 1 and dadX BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit dadX, a GAM353678 bacterial target gene which is associated with Escherichia coli CFT073 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Escherichia coli CFT073 infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	def	Chlamydomon hila pneu moniae CW L029	GAM353678 is a human miRNA-like oligonucleotide, which targets Polypeptide Deformylase (def, NC_000922 from 1221735 to 1222295 (+)), a bacterial target gene encoded by the Chlamydomon hila pneumoniae CWL029 genome, as part of an anti-bacterial host defense mechanism. def BINDING SITE 1 and def BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the def gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of def BINDING SITE 1 and def BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit def, a GAM353678 bacterial target gene which is associated with Chlamydomon hila pneumoniae CWL029 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Chlamydomon hila pneumoniae CWL029 infection and associated clinical conditions.	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	def	Chlamydom hila pneu moniae J1 38	GAM353678 is a human miRNA-like oligonucleotide, which targets polypeptide deformylase (def, NC_002491 from 1218069 to 1218629 (+)), a bacterial target gene encoded by the Chlamydomon hila pneumoniae J138 genome, as part of an anti-bacterial host defense mechanism. def BINDING SITE 1 and def BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the def gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of def BINDING SITE 1 and def BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit def, a GAM353678 bacterial target gene which is associated	A

GAM35 3678	CAGCAGCA CACTGTGG TTTGTA	Human	dnaE	Mycobacterium leprae	with <i>Chlamydomonas reinhardtii</i> J138 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Chlamydomonas reinhardtii</i> J138 infection and associated clinical conditions	A
GAM35 3678	CAGCAGCA CACTGTGG TTTGTA	Human	dsdA	Salmonella typhimurium LT2	GAM353678 is a human miRNA-like oligonucleotide, which targets DNA polymerase III, [alpha] subunit (dnaE, NC_002677 from 1423014 to 1426547 (+)), a bacterial target gene encoded by the <i>Mycobacterium leprae</i> genome, as part of an anti-bacterial host defense mechanism. dnaE BINDING SITE 1 through dnaE BINDING SITE 3 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the dnaE gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of dnaE BINDING SITE 1 through dnaE BINDING SITE 3, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit dnaE, a GAM353678 bacterial target gene which is associated with <i>Mycobacterium leprae</i> infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Mycobacterium leprae</i> infection and associated clinical conditions	A
GAM35 3678	CAGCAGCA CACTGTGG TTTGTA	Human	fepC	Pseudomonas aeruginosa PA01	GAM353678 is a human miRNA-like oligonucleotide, which targets D-serine deaminase (dsdA, NC_003197 from 4004453 to 4005775 (+)), a bacterial target gene encoded by the <i>Salmonella typhimurium</i> LT2 genome, as part of an anti-bacterial host defense mechanism. dsdA BINDING SITE 1 and dsdA BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the dsdA gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of dsdA BINDING SITE 1 and dsdA BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit dsdA, a GAM353678 bacterial target gene which is associated with <i>Salmonella typhimurium</i> LT2 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Salmonella typhimurium</i> LT2 infection and associated clinical conditions	A
GAM35 3678	CAGCAGCA CACTGTGG TTTGTA	Human	fepC	Pseudomonas aeruginosa PA01	GAM353678 is a human miRNA-like oligonucleotide, which targets ferric enterobactin transport protein FepC (fepC, NC_002516 from 4653508 to 4654305 (-)), a bacterial target gene encoded by the <i>Pseudomonas aeruginosa</i> PA01 genome, as	A

				part of an anti-bacterial host defense mechanism. fepC BINDING SITE 1 and fepC BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the fepC gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of fepC BINDING SITE 1 and fepC BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit fepC, a bacterial target gene which is associated with Pseudomonas aeruginosa PA01 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Pseudomonas aeruginosa PA01 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human fhaL	Bordetella pertussis is	GAM353678 is a human miRNA-like oligonucleotide, which targets adhesin (fhaL, NC_002929 from 3085865 to 3098455 (+)), a bacterial target gene encoded by the Bordetella pertussis genome, as part of an anti-bacterial host defense mechanism. fhaL BINDING SITE 1 and fhaL BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the fhaL gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of fhaL BINDING SITE 1 and fhaL BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit fhaL, a bacterial target gene which is associated with Bordetella pertussis infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Bordetella pertussis infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human flhB	Bordetella pertussis is	GAM353678 is a human miRNA-like oligonucleotide, which targets flagellar biosynthetic protein FlhB (flhB, NC_002929 from 1441767 to 1442921 (+)), a bacterial target gene encoded by the Bordetella pertussis genome, as part of an anti-bacterial host defense mechanism. flhB BINDING SITE 1 through flhB BINDING SITE 3 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the flhB gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of flhB BINDING SITE 1 through flhB BINDING SITE 3, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby	A

GAM35 3678	CAGCAGCA CACTGTGG TTTGTA	Human	fmtB(Staphylococcus aureus subsp. aureus N315	incorporated herein. Another function of GAM353678 is to inhibit fHb, a GAM353678 bacterial target gene which is associated with <i>Bordetella pertussis</i> infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Bordetella pertussis</i> infection and associated clinical conditions	A
GAM35 3678	CAGCAGCA CACTGTGG TTTGTA	Human	fmtB(Staphylococcus aureus subsp. aureus Mu50	GAM353678 is a human miRNA-like oligonucleotide, which targets FmtB protein (fmtB(mrp), NC_002745 from 2218145 to 2225590 (-)), a bacterial target gene encoded by the <i>Staphylococcus aureus</i> subsp. aureus N315 genome, as part of an anti-bacterial host defense mechanism. fmtB(mrp) BINDING SITE 1 and fmtB(mrp) BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the fmtB(mrp) gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of fmtB(mrp) BINDING SITE 1 and fmtB(mrp) BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit fmtB(mrp), a GAM353678 bacterial target gene which is associated with <i>Staphylococcus aureus</i> subsp. aureus N315 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Staphylococcus aureus</i> subsp. aureus N315 infection and associated clinical conditions	A
GAM35 3678	CAGCAGCA CACTGTGG TTTGTA	Human	fmtB(Staphylococcus aureus subsp. aureus Mu50	GAM353678 is a human miRNA-like oligonucleotide, which targets FmtB protein (fmtB(mrp), NC_002758 from 2287935 to 2295380 (-)), a bacterial target gene encoded by the <i>Staphylococcus aureus</i> subsp. aureus Mu50 genome, as part of an anti-bacterial host defense mechanism. fmtB(mrp) BINDING SITE 1 and fmtB(mrp) BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the fmtB(mrp) gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of fmtB(mrp) BINDING SITE 1 and fmtB(mrp) BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit fmtB(mrp), a GAM353678 bacterial target gene which is associated with <i>Staphylococcus aureus</i> subsp. aureus Mu50 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Staphylococcus aureus</i> subsp.	A

					aureus Mu50 infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	ftsY	Chlamydomonas hila pneumoniae J138	GAM353678 is a human miRNA-like oligonucleotide, which targets cell division protein ftsY (ftsY, NC_002491 from 1113127 to 1113999 (-)), a bacterial target gene encoded by the Chlamydomonas pneumoniae J138 genome, as part of an anti-bacterial host defense mechanism. ftsY BINDING SITE 1 and ftsY BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the ftsY gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of ftsY BINDING SITE 1 and ftsY BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit ftsY, a GAM353678 bacterial target gene which is associated with Chlamydomonas pneumoniae J138 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Chlamydomonas pneumoniae J138 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	ftsY	Chlamydomonas hila pneumoniae CWL029	GAM353678 is a human miRNA-like oligonucleotide, which targets Cell Division Protein FtsY (ftsY, NC_000922 from 1115427 to 1116299 (-)), a bacterial target gene encoded by the Chlamydomonas pneumoniae CWL029 genome, as part of an anti-bacterial host defense mechanism. ftsY BINDING SITE 1 and ftsY BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the ftsY gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of ftsY BINDING SITE 1 and ftsY BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit ftsY, a GAM353678 bacterial target gene which is associated with Chlamydomonas pneumoniae CWL029 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Chlamydomonas pneumoniae CWL029 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	gad	Pseudomonas putida KT2440	GAM353678 is a human miRNA-like oligonucleotide, which targets guanine aminohydrolase (gad, NC_002947 from 4871625 to 4872929 (+)), a bacterial target gene encoded by the Pseudomonas putida KT2440 genome, as part of an anti-bacterial host defense mechanism. gad BINDING SITE 1 and gad BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA	A

				encoded by the gad gene, corresponding to target binding sites such as BINDING SITE 1, BINDING SITE II or BINDING SITE I II of Fig. 1. The nucleotide sequences of gad BINDING SITE 1 and gad BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit gad, a GAM353678 bacterial target gene which is associated with <i>Pseudomonas putida</i> KT2440 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Pseudomonas putida</i> KT 2440 infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human glaC	<i>Escherichia coli</i> CFT073	GAM353678 is a human miRNA-like oligonucleotide, which targets <i>Glc operon</i> transcriptional activator (<i>glcC</i> , NC_004431 from 3542871 to 3543695 (+)), a bacterial target gene encoded by the <i>Escherichia coli</i> CFT073 genome, as part of an anti-bacterial host defense mechanism. <i>glcC</i> BINDING SITE 1 and <i>glcC</i> BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the <i>glcC</i> gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of <i>glcC</i> BINDING SITE 1 and <i>glcC</i> BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit <i>glcC</i> , a GAM353678 bacterial target gene which is associated with <i>Escherichia coli</i> CFT073 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Escherichia coli</i> CFT073 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human glgP	<i>Salmonella enterica enterica</i> serovar Typhi Ty2	GAM353678 is a human miRNA-like oligonucleotide, which targets <i>glycogen phosphorylase</i> (<i>glgP</i> , NC_004631 from 4129215 to 4131662 (+)), a bacterial target gene encoded by the <i>Salmonella enterica enterica</i> serovar Typhi Ty2 genome, as part of an anti-bacterial host defense mechanism. <i>glgP</i> BINDING SITE 1 and <i>glgP</i> BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the <i>glgP</i> gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of <i>glgP</i> BINDING SITE 1 and <i>glgP</i> BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit <i>glgP</i> , a GAM353678 bacterial target gene which is associated with <i>Salmonella enterica enterica</i> serovar	A

					<p>Typhi Ty2 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Salmonella enterica enterica</i> serovar Typhi Ty2 infection and associated clinical conditions</p>	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	glgP	<p><i>Salmonella enterica enterica</i> serovar Typhi</p>	<p>GAM353678 is a human miRNA-like oligonucleotide, which targets glycogen phosphorylase (glgP, NC_003198 from 4144568 to 4147015 (+)), a bacterial target gene encoded by the <i>Salmonella enterica enterica</i> serovar Typhi genome, as part of an anti-bacterial host defense mechanism. glgP BINDING SITE 1 and glgP BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the glgP gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of glgP BINDING SITE 1 and glgP BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit glgP, a GAM353678 bacterial target gene which is associated with <i>Salmonella enterica enterica</i> serovar Typhi infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Salmonella enterica enterica</i> serovar Typhi infection and associated clinical conditions</p>	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	glpC	<p><i>Yersinia pestis</i> KIM</p>	<p>GAM353678 is a human miRNA-like oligonucleotide, which targets sn-glycerol-3-phosphate dehydrogenase (anaerobic), K-small subunit (glpC, NC_004088 from 454677 to 456047 (+)), a bacterial target gene encoded by the <i>Yersinia pestis</i> KIM genome, as part of an anti-bacterial host defense mechanism. glpC BINDING SITE 1 and glpC BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the glpC gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of glpC BINDING SITE 1 and glpC BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit glpC, a GAM353678 bacterial target gene which is associated with <i>Yersinia pestis</i> KIM infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Yersinia pestis</i> KIM infection and associated clinical conditions</p>	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	glpC	<p><i>Yersinia pestis</i></p>	<p>GAM353678 is a human miRNA-like oligonucleotide, which targets anaerobic glycerol-3-phosphate dehydrogenase subunit</p>	A

				<p>C (glpC, NC_003143 from 4289650 to 4290897 (-)), a bacterial target gene encoded by the <i>Yersinia pestis</i> genome, as part of an anti-bacterial host defense mechanism. glpC BINDING SITE 1 and glpC BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the glpC gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of glpC BINDING SITE 1 and glpC BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit glpC, a GAM353678 bacterial target gene which is associated with <i>Yersinia pestis</i> infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Yersinia pestis</i> infection and associated clinical conditions</p>	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	glpD Brucella suis 1330	<p>GAM353678 is a human miRNA-like oligonucleotide, which targets glycerol-3-phosphate dehydrogenase (glpD, NC_004310 from 210763 to 212274 (+)), a bacterial target gene encoded by the <i>Brucella suis</i> 1330 genome, as part of an anti-bacterial host defense mechanism. glpD BINDING SITE 1 and glpD BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the glpD gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of glpD BINDING SITE 1 and glpD BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit glpD, a GAM353678 bacterial target gene which is associated with <i>Brucella suis</i> 1330 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Brucella suis</i> 1330 infection and associated clinical conditions</p>	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	ipaH_5 Shigella flexneri 2a str. 2457T	<p>GAM353678 is a human miRNA-like oligonucleotide, which targets invasion plasmid antigen (ipaH_5, NC_004741 from 2023205 to 2024848 (+)), a bacterial target gene encoded by the <i>Shigella flexneri</i> 2a str. 2457T genome, as part of an anti-bacterial host defense mechanism. ipaH_5 BINDING SITE 1 and ipaH_5 BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the ipaH_5 gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of ipaH_5 BINDING SITE 1 and ipaH_5 BINDING SITE 2, and the</p>	A

GAM35 CAGCAGCA Human ipaH9 Shigella
3678 CACTGTGG .8 flexneri
TTTGTA 2a str. 3
01

complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit ipaH_{9.8}, a GAM353678 bacterial target gene which is associated with *Shigella flexneri* 2a str. 2457T infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of *Shigella flexneri* 2a str. 2457T infection and associated clinical conditions.

GAM353678 is a human miRNA-like oligonucleotide, which targets invasion plasmid antigen (ipaH_{9.8}, NC_004337 from 1422064 to 1423779 (-)), a bacterial target gene encoded by the *Shigella flexneri* 2a str. 301 genome, as part of an anti-bacterial host defense mechanism. ipaH_{9.8} BINDING SITE I and ipaH_{9.8} BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the ipaH_{9.8} gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of ipaH_{9.8} BINDING SITE I and ipaH_{9.8} BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit ipaH_{9.8}, a GAM353678 bacterial target gene which is associated with *Shigella flexneri* 2a str. 301 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of *Shigella flexneri* 2a str. 301 infection and associated clinical conditions.

GAM35 CAGCAGCA Human livH Bordetella
3678 CACTGTGG a pertussis
TTTGTA is

GAM353678 is a human miRNA-like oligonucleotide, which targets high-affinity branched-chain amino acid transport system permease protein (livH, NC_002929 from 1144729 to 1145607 (+)), a bacterial target gene encoded by the *Bordetella pertussis* genome, as part of an anti-bacterial host defense mechanism. livH BINDING SITE is a bacterial target binding site that is found in the 3' untranslated region of mRNA encoded by the livH gene, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of livH BINDING SITE, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit livH, a GAM353678 bacterial target gene which is associated with *Bordetella pertussis* infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and

					treatment of <i>Bordetella pertussis</i> infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTG	Human	lppI	Mycobacterium tuberculosis H37Rv	GAM353678 is a human miRNA-like oligonucleotide, which targets lppI (lppI, NC_000962 from 2291267 to 2291923 (+)), a bacterial target gene encoded by the <i>Mycobacterium tuberculosis</i> H37Rv genome, as part of an anti-bacterial host defense mechanism. lppI BINDING SITE 1 and lppI BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the lppI gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of lppI BINDING SITE 1 and lppI BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit lppI, a GAM353678 bacterial target gene which is associated with <i>Mycobacterium tuberculosis</i> H37Rv infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Mycobacterium tuberculosis</i> H37Rv infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTG	Human	lppI	Mycobacterium bovis subsp. bovis AF2122/97	GAM353678 is a human miRNA-like oligonucleotide, which targets Probable lipoprotein lppI (lppI, NC_002945 from 2275182 to 2275838 (+)), a bacterial target gene encoded by the <i>Mycobacterium bovis</i> subsp. bovis AF2122/97 genome, as part of an anti-bacterial host defense mechanism. lppI BINDING SITE 1 and lppI BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the lppI gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of lppI BINDING SITE 1 and lppI BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit lppI, a GAM353678 bacterial target gene which is associated with <i>Mycobacterium bovis</i> subsp. bovis AF2122/97 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM 353678 include the diagnosis, prevention and treatment of <i>Mycobacterium bovis</i> subsp. bovis AF2122/97 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTG	Human	MGAT5	Human	GAM353678 is a human miRNA-like oligonucleotide, which targets a human mannosyl (alpha-1,6-)-glycoprotein beta-1,6-N-acetylglucosaminyltransferase (MGAT5, Accession number: NM_002410) as part of a host response mechanism associated with a <i>Salmonella typhimurium</i> LT2 infection. MGAT5 BINDING SITE is a human target binding site that is a focus	A

					<p>in the the 3' untranslated region of mRNA encoded by the MGAT5 gene, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. Additionally, using the binding site prediction system of the present invention GAM353678-A binds to sequences on orthologous UTR of rat (NM_023095). The nucleotide sequences of MGAT5 BINDING SITE, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit MGAT5, a GAM353678 human target gene which encodes an enzyme that catalyzes beta 1-6 branching on N-linked carbohydrates. MGAT5 is associated with Salmonella typhimurium LT2 infection, and therefore GAM353678 is associated with the abovementioned infection, as part of a host response mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Salmonella typhimurium LT2 infection and associated clinical conditions. The function of MGAT5 and its association with various diseases and clinical conditions has been established by previous studies, as described hereinabove with reference to GAM3451.</p>	A
GAM353678	CAGCAGCA CACTGTGG TTTGTGTA	Human	miaA	Chlamydia trachomatis	<p>GAM353678 is a human miRNA-like oligonucleotide, which targets tRNA isopentenylpyrophosphate transferase (miaA, NC_000117 from 899276 to 900295 (+)), a bacterial target gene encoded by the Chlamydia trachomatis genome, as part of an anti-bacterial host defense mechanism. miaA BINDING SITE 1 and miaA BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the miaA gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of miaA BINDING SITE 1 and miaA BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit miaA, a GAM353678 bacterial target gene which is associated with Chlamydia trachomatis infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Chlamydia trachomatis infection and associated clinical conditions.</p>	
GAM353678	CAGCAGCA CACTGTGG TTTGTGTA	Human	minE	Pseudomonas putida KT2440	<p>GAM353678 is a human miRNA-like oligonucleotide, which targets cell division topological specificity factor MinE (minE, NC_002947 from 1932680 to 1932934 (-)), a bacterial target gene encoded by the Pseudomonas putida KT2440 genome, as part of an anti-bacterial host defense mechanism. minE BINDING SITE is a bacterial target binding site that is found in the the 3' untranslated region</p>	A

					<p>of mRNA encoded by the <i>minE</i> gene, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of <i>minE</i> BINDING SITE, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit <i>minE</i>, a GAM353678 bacterial target gene which is associated with <i>Pseudomonas putida</i> KT2440 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Pseudomonas putida</i> KT2440 infection and associated clinical conditions</p>	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	<i>nicT</i>	<i>Mycobacterium tuberculosis</i> H37Rv	<p>GAM353678 is a human miRNA-like oligonucleotide, which targets <i>nicT</i> (<i>nicT</i>, NC_000962 from 3166681 to 3167799 (+)), a bacterial target gene encoded by the <i>Mycobacterium tuberculosis</i> H37Rv genome, as part of an anti-bacterial host defense mechanism. <i>nicT</i> BINDING SITE 1 and <i>nicT</i> BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the <i>nicT</i> gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of <i>nicT</i> BINDING SITE 1 and <i>nicT</i> BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit <i>nicT</i>, a GAM353678 bacterial target gene which is associated with <i>Mycobacterium tuberculosis</i> H37Rv infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Mycobacterium tuberculosis</i> H37Rv infection and associated clinical conditions</p>	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	<i>nicT</i>	<i>Mycobacterium bovis</i> subsp. <i>bovis</i> AF2122/97	<p>GAM353678 is a human miRNA-like oligonucleotide, which targets POSSIBLE NICKEL-TRANSPORT INTEGRAL MEMBRANE PROTEIN NICT (<i>nicT</i>, NC_002945 from 3123200 to 3124318 (+)), a bacterial target gene encoded by the <i>Mycobacterium bovis</i> subsp. <i>bovis</i> AF2122/97 genome, as part of an anti-bacterial host defense mechanism. <i>nicT</i> BINDING SITE 1 and <i>nicT</i> BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the <i>nicT</i> gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of <i>nicT</i> BINDING SITE 1 and <i>nicT</i> BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit <i>nicT</i>, a GAM353678 bacterial target gene which is associated</p>	A

				with <i>Mycobacterium b ovis</i> subsp <i>bovis</i> AF2122/97 infection, as part of an anti-bacte rial host defense mechanism. Accordingly, the utilities of GAM 353678 include the diagnosis, prevention and treatment of Myco bacterium <i>bovis</i> subsp <i>bovis</i> AF2122/97 infection and associated clinical conditions		
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	nupC	Shigella flexneri 2a str. 301	GAM353678 is a human miRNA-like oligonucleotide, which targets permease of transport system for 3 nucleosides (nupC, NC_004337 from 2515842 to 2517083 (+)), a bacterial target gene encoded by the <i>Shigella flexneri</i> 2a str. 301 genome, as part of an anti-bacterial host defense mechanism. nupC BINDING SITE 1 through nupC BINDING SITE 3 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the nupC gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of nupC BINDING SITE 1 through nupC BINDING SITE 3, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit nupC, a GAM353678 bacterial target gene which is associated with <i>Shigella flexneri</i> 2a str. 301 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Shigella flexneri</i> 2a str. 301 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	nupC	Escherichia coli CFT073	GAM353678 is a human miRNA-like oligonucleotide, which targets Nucleoside permease nupC (nupC, NC_004431 from 2795390 to 2796631 (+)), a bacterial target gene encoded by the <i>Escherichia coli</i> CFT073 genome, as part of an anti-bacterial host defense mechanism. nupC BINDING SITE 1 through nupC BINDING SITE 3 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the nupC gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of nupC BINDING SITE 1 through nupC BINDING SITE 3, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit nupC, a GAM353678 bacterial target gene which is associated with <i>Escherichia coli</i> CFT073 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Escherichia coli</i> CFT073 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	nupC	Shigella flexneri 2a str. 2	GAM353678 is a human miRNA-like oligonucleotide, which targets permease of transport system for 3 nucleosides	A

457T						(nupC, NC_00447.41 from 2494019 to 2495221 (+)), a bacterial target gene encoded by the <i>Shigella flexneri</i> 2a str. 2457T genome, as part of an anti-bacterial host defense mechanism. nupC BINDING SITE 1 through nupC BINDING SITE 3 are bacterial target binding sites that are found in the untranslated region of mRNA encoded by the nupC gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of nupC BINDING SITE 1 through nupC BINDING SITE 3, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit nupC, a GAM353678 bacterial target gene which is associated with <i>Shigella flexneri</i> 2a str. 2457T infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Shigella flexneri</i> 2a str. 2457T infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	ompG	Escherichia coli CFT073		GAM353678 is a human miRNA-like oligonucleotide, which targets Outer membrane protein G precursor (ompG, NC_004431 from 16 24577 to 1625533 (+)), a bacterial target gene encoded by the <i>Escherichia coli</i> CFT073 genome, as part of an anti-bacterial host defense mechanism. ompG BINDING SITE 1 and ompG BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the ompG gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of ompG BINDING SITE 1 and ompG BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit ompG, a GAM353678 bacterial target gene which is associated with <i>Escherichia coli</i> CFT073 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Escherichia coli</i> CFT073 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	orn	Yersinia pestis		GAM353678 is a human miRNA-like oligonucleotide, which targets oligoribonuclease (orn, NC_003143 from 378331 to 378876 (+)), a bacterial target gene encoded by the <i>Yersinia pestis</i> genome, as part of an anti-bacterial host defense mechanism. orn BINDING SITE 1 is a bacterial target binding site that is found in the 3' untranslated region of mRNA encoded by the orn gene, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of orn BINDING SITE,	A

GAM353678 CAGCAGCA CACTGTGG TTTGTA	Human oxyR	Salmonella enterica enterica serovar Typhi	<p>and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit orn, a GAM353678 bacterial target gene which is associated with <i>Yersinia pestis</i> infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Yersinia pestis</i> infection and associated clinical conditions</p>	A
GAM353678 CAGCAGCA CACTGTGG TTTGTA	Human oxyR	Salmonella typhimurium LT2	<p>GAM353678 is a human miRNA-like oligonucleotide, which targets hydrogen peroxide-inducible regulon activator (oxyR, NC_003198 from 3607204 to 3608121 (-)), a bacterial target gene encoded by the <i>Salmonella enterica enterica</i> serovar Typhi genome, as part of an anti-bacterial host defense mechanism. oxyR BINDING SITE 1 and oxyR BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the oxyR gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of oxyR BINDING SITE 1 and oxyR BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit oxyR, a GAM353678 bacterial target gene which is associated with <i>Salmonella enterica enterica</i> serovar Typhi infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Salmonella enterica enterica</i> serovar Typhi infection and associated clinical conditions</p> <p>GAM353678 is a human miRNA-like oligonucleotide, which targets oxidative stress regulatory protein (oxyR, NC_003197 from 4343080 to 4343997 (+)), a bacterial target gene encoded by the <i>Salmonella typhimurium</i> LT2 genome, as part of an anti-bacterial host defense mechanism. oxyR BINDING SITE 1 and oxyR BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the oxyR gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of oxyR BINDING SITE 1 and oxyR BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit oxyR, a GAM353678 bacterial target gene which is associated with <i>Salmonella typhimurium</i> LT2 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Salmonella typhimurium</i> LT2 infection and</p>	A

					associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	oxyR	Salmonella enterica serovar Typhi Ty2	GAM353678 is a human miRNA-like oligonucleotide, which targets hydrogen peroxide-inducible regulon activator (oxyR, NC_004631.1 from 3592864 to 3593781 (-)), a bacterial target gene encoded by the <i>Salmonella enterica enterica</i> serovar Typhi Ty2 genome, as part of an anti-bacterial host defense mechanism. oxyR BINDING SITE 1 and oxyR BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the oxyR gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of oxyR BINDING SITE 1 and oxyR BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit oxyR, a GAM353678 bacterial target gene which is associated with <i>Salmonella enterica enterica</i> serovar Typhi Ty2 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Salmonella enterica enterica</i> serovar Typhi Ty2 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	pbpG	<i>Pseudomonas putida</i> KT2440	GAM353678 is a human miRNA-like oligonucleotide, which targets D-alanyl-D-alanine-endopeptidase (pbpG, NC_002947 from 4323707 to 4324633 (+)), a bacterial target gene encoded by the <i>Pseudomonas putida</i> KT2440 genome, as part of an anti-bacterial host defense mechanism. pbpG BINDING SITE 1 and pbpG BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the pbpG gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of pbpG BINDING SITE 1 and pbpG BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit pbpG, a GAM353678 bacterial target gene which is associated with <i>Pseudomonas putida</i> KT2440 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Pseudomonas putida</i> KT2440 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	pchA	<i>Pseudomonas aeruginosa</i> PA01	GAM353678 is a human miRNA-like oligonucleotide, which targets salicylate biosynthesis isochorismate synthase (pchA, NC_002516 from 4745120 to 4746350 (+)), a bacterial target gene encoded by the <i>Pseudomonas aeruginosa</i> PA01 genome, as part of an anti-bacterial host defense mechanism. pchA BINDING SITE 1 and pchA BINDING SITE 2 are bacterial target	A

					binding sites that are found in the untranslated regions of mRNA encoded by the <i>pcnA</i> gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of <i>pcnA</i> BINDING SITE 1 and <i>pcnA</i> BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit <i>pcnA</i> , a GAM353678 bacterial target gene which is associated with <i>Pseudomonas aeruginosa</i> PA01 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Pseudomonas aeruginosa</i> PA01 infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	<i>pcnA</i>	<i>Mycobacterium leprae</i>	GAM353678 is a human miRNA-like oligonucleotide, which targets <i>pcnA</i> (<i>pcnA</i> , NC_002677 from 3248268 to 3249728 (-)), a bacterial target gene encoded by the <i>Mycobacterium leprae</i> genome, as part of an anti-bacterial host defense mechanism. <i>pcnA</i> BINDING SITE 1 and <i>pcnA</i> BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the <i>pcnA</i> gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of <i>pcnA</i> BINDING SITE 1 and <i>pcnA</i> BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit <i>pcnA</i> , a GAM353678 bacterial target gene which is associated with <i>Mycobacterium leprae</i> infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Mycobacterium leprae</i> infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	<i>phnV</i>	<i>Salmonella enterica</i> serovar Typhi	GAM353678 is a human miRNA-like oligonucleotide, which targets probable membrane component of 2-aminoethylphosphonate transporter (<i>phnV</i> , NC_003198 from 471575 to 472366 (-)), a bacterial target gene encoded by the <i>Salmonella enterica</i> serovar Typhi genome, as part of an anti-bacterial host defense mechanism. <i>phnV</i> BINDING SITE 1 and <i>phnV</i> BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the <i>phnV</i> gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of <i>phnV</i> BINDING SITE 1 and <i>phnV</i> BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit <i>phnV</i> , a GAM353678	A

<p>GAM353678 CAGCAGCA CACTGTGG TTTGTA</p>	<p>Human phnV</p>	<p>Salmonella enterica enterica serovar Typhi Ty2</p>	<p>bacterial target gene which is associated with <i>Salmonella enterica enterica</i> serovar Typhi infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Salmonella enterica enterica</i> serovar Typhi infection and associated clinical conditions</p> <p>GAM353678 is a human miRNA-like oligonucleotide, which targets probable membrane component of 2-aminoethylphosphonate transporter (phnV, NC_004631 from 2508735 to 2509526 (+)), a bacterial target gene encoded by the <i>Salmonella enterica enterica</i> serovar Typhi Ty2 genome, as part of an anti-bacterial host defense mechanism. phnV BINDING SITE 1 and phnV BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the phnV gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of phnV BINDING SITE 1 and phnV BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit phnV, a GAM353678 bacterial target gene which is associated with <i>Salmonella enterica enterica</i> serovar Typhi Ty2 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Salmonella enterica enterica</i> serovar Typhi Ty2 infection and associated clinical conditions</p>	<p>A</p>
<p>GAM353678 CAGCAGCA CACTGTGG TTTGTA</p>	<p>Human phoY2</p>	<p>Mycobacterium bovis subsp bovis AF2122/97</p>	<p>GAM353678 is a human miRNA-like oligonucleotide, which targets PROBABLE PHOSPHATE-TRANSPORT SYSTEM TRANSCRIPTIONAL REGULATOR Y PROTEIN phoY2 (phoY2, NC_002945 from 914388 to 915029 (-)), a bacterial target gene encoded by the <i>Mycobacterium bovis</i> subsp bovis AF2122/97 genome, as part of an anti-bacterial host defense mechanism. phoY2 BINDING SITE 1 and phoY2 BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the phoY2 gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of phoY2 BINDING SITE 1 and phoY2 BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit phoY2, a GAM353678 bacterial target gene which is associated with <i>Mycobacterium bovis</i> subsp bovis AF2122/97 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Mycobacterium bovis</i> subsp bovis AF2122/97 infection and associated</p>	<p>A</p>

				clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	phoY2	Mycobacterium tuberculosis H37Rv	A
				GAM353678 is a human miRNA-like oligonucleotide, which targets phoY2 (phoY2, NC_000962 from 913556 to 914197 (-)), a bacterial target gene encoded by the Mycobacterium tuberculosis H37Rv genome, as part of an anti-bacterial host defense mechanism. phoY2 BINDING SITE 1 and phoY2 BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the phoY2 gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of phoY2 BINDING SITE 1 and phoY2 BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit phoY2, a bacterial target gene which is associated with Mycobacterium tuberculosis H37Rv infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Mycobacterium tuberculosis H37Rv infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	pilT	Pseudomonas putida KT2440	A
				GAM353678 is a human miRNA-like oligonucleotide, which targets type IV pilT twitching motility protein PilT (pilT, NC_002947 from 5816934 to 5817944 (-)), a bacterial target gene encoded by the Pseudomonas putida KT2440 genome, as part of an anti-bacterial host defense mechanism. pilT BINDING SITE 1 through pilT BINDING SITE 3 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the pilT gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of pilT BINDING SITE 1 through pilT BINDING SITE 3, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit pilT, a bacterial target gene which is associated with Pseudomonas putida KT2440 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Pseudomonas putida KT2440 infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	polA	Mycobacterium leprae	A
				GAM353678 is a human miRNA-like oligonucleotide, which targets DNA polymerase I (polA, NC_002677 from 1648220 to 1650955 (-)), a bacterial target gene encoded by the Mycobacterium leprae genome, as part of an anti-bacterial host defense mechanism. polA BINDING SITE 1 and polA BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the polA gene, corresponding to target binding sites such as BINDING SITE I,	

<p>GAM353678 CAGCAGCA CACTGTGG TTTGTA</p>	<p>Human prcA</p>	<p>Mycobacterium leprae</p>	<p>BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of polA BINDING SITE 1 and polA BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit polA, a GAM353678 bacterial target gene which is associated with Mycobacterium leprae infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Mycobacterium leprae infection and associated clinical conditions</p>	<p>A</p>
<p>GAM353678 CAGCAGCA CACTGTGG TTTGTA</p>	<p>Human pta</p>	<p>Pseudomonas putida KT2440</p>	<p>GAM353678 is a human miRNA-like oligonucleotide, which targets proteasome [alpha]-type subunit 1 (prcA, NC_002677 from 1576553 to 1577350 (+)), a bacterial target gene encoded by the Mycobacterium leprae genome, as part of an anti-bacterial host defense mechanism. prcA BINDING SITE 1 and prcA BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the prcA gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of prcA BINDING SITE 1 and prcA BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit prcA, a GAM353678 bacterial target gene which is associated with Mycobacterium leprae infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Mycobacterium leprae infection and associated clinical conditions</p>	<p>A</p>
<p>GAM353678 CAGCAGCA CACTGTGG TTTGTA</p>	<p>Human pta</p>	<p>Pseudomonas putida KT2440</p>	<p>GAM353678 is a human miRNA-like oligonucleotide, which targets phosphate acetyltransferase (pta, NC_002947 from 891625 to 893712 (-)), a bacterial target gene encoded by the Pseudomonas putida KT2440 genome, as part of an anti-bacterial host defense mechanism. pta BINDING SITE 1 and pta BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the pta gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of pta BINDING SITE 1 and pta BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit pta, a GAM353678 bacterial target gene which is associated with Pseudomonas putida KT2440 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis,</p>	<p>A</p>

					prevention and treatment of <i>Pseudomonas putida</i> KT 2440 infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	ptsH	Salmonella enterica serovar Typhi	GAM353678 is a human miRNA-like oligonucleotide, which targets phosphocarrier protein HPr (ptsH, NC_003198 from 2505403 to 2505660 (+)), a bacterial target gene encoded by the <i>Salmonella enterica</i> serovar Typhi genome, as part of an anti-bacterial host defense mechanism. ptsH BINDING SITE is a bacterial target binding site that is found in the 3' untranslated region of mRNA encoded by the ptsH gene, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of ptsH BINDING SITE, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit ptsH, a bacterial target gene which is associated with <i>Salmonella enterica</i> serovar Typhi infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Salmonella enterica</i> serovar Typhi infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	rbsR	Shigella flexneri 2a str. 301	GAM353678 is a human miRNA-like oligonucleotide, which targets regulator for rbs operon (rbsR, NC_004337 from 3947708 to 3948700 (+)), a bacterial target gene encoded by the <i>Shigella flexneri</i> 2a str. 301 genome, as part of an anti-bacterial host defense mechanism. rbsR BINDING SITE 1 through rbsR BINDING SITE 3 are bacterial target binding sites that are found in the untranslated region of mRNA encoded by the rbsR gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of rbsR BINDING SITE 1 through rbsR BINDING SITE 3, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit rbsR, a bacterial target gene which is associated with <i>Shigella flexneri</i> 2a str. 301 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Shigella flexneri</i> 2a str. 301 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	rbsR	Shigella flexneri 2a str. 2457T	GAM353678 is a human miRNA-like oligonucleotide, which targets regulator for rbs operon (rbsR, NC_004741 from 3824594 to 3825577 (-)), a bacterial target gene encoded by the <i>Shigella flexneri</i> 2a str. 2457T genome, as part of an anti-bacterial host defense mechanism. rbsR BINDING SITE 1 through rbsR BINDING SITE 3 are bacterial target binding sites	A

				that are found in the untranslated region s of mRNA encoded by the rbsR gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of rbsR BINDING SITE 1 through rbsR BINDING SITE 3, and the complementary seco ndary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit rbsR, a GAM353678 bacterial target gene which is associated with Shigella flexneri 2a str. 2457T infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Shigella flexneri 2a str. 2457T infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human rbsR	Escherichia coli CFT073	GAM353678 is a human miRNA-like oligonucleotide, which targets Ribose operon repressor (rbsR, NC_004431 from 4439260 to 44 40252 (-)), a bacterial target gene encoded by the Escherichia coli CFT073 genome, as part of an anti-bacterial host defense mechanism. rbsR BINDING SITE 1 through rbsR BINDING SITE 3 are bacterial target binding sites that are found in the untranslated region s of mRNA encoded by the rbsR gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig.1. The nucleotide sequences of rbsR BINDING SITE 1 through rbsR BINDING SITE 3, and the complementary seco ndary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit rbsR, a GAM353678 bacterial target gene which is associated with Escherichia coli CFT073 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Escherichia coli CFT073 infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human recG	Mycobacterium leprae	GAM353678 is a human miRNA-like oligonucleotide, which targets ATP-dependent DNA helicase (recG, NC_002677 from 2014723 to 2016954 (-)), a bacterial target gene encoded by the Mycobacterium leprae genome, as part of an anti-bacterial host defense mechanism. recG BINDING SITE 1 and recG BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the recG gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of recG BINDING SITE 1 and recG BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit recG, a GAM353678	A

GAM353678 CAGCAGCA CACTGTGG TTTGTGTA	Human	relA	Mycobacterium bovis AF2122/97	<p>bacterial target gene which is associated with Mycobacterium leprae infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Mycobacterium leprae infection and associated clinical conditions</p> <p>GAM353678 is a human miRNA-like oligonucleotide, which targets PROBABLE GTP PYROPHOSPHOKINASE RELA (ATP:GTP 3'-PYROPHOSPHOTRANSFERASE) (PPGPP SYNTHETASE I) ((P)PPGPP SYNTHETASE) (GTP DIPYROPHOSPHOKINASE) (relA, NC_002945 from 2875274 to 2877646 (-)), a bacterial target gene encoded by the Mycobacterium bovis subsp bovis AF2122/97 genome, as part of an anti-bacterial host defense mechanism. relA BINDING SITE 1 and relA BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the relA gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of relA BINDING SITE 1 and relA BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit relA, a GAM353678 bacterial target gene which is associated with Mycobacterium bovis subsp bovis AF2122/97 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM 353678 include the diagnosis, prevention and treatment of Mycobacterium bovis subsp bovis AF2122/97 infection and associated clinical conditions</p>	A
GAM353678 CAGCAGCA CACTGTGG TTTGTGTA	Human	relA	Mycobacterium tuberculosis H37Rv	<p>GAM353678 is a human miRNA-like oligonucleotide, which targets relA (relA, NC_000962 from 2907824 to 2910196 (-)), a bacterial target gene encoded by the Mycobacterium tuberculosis H37Rv genome, as part of an anti-bacterial host defense mechanism. relA BINDING SITE 1 and relA BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the relA gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of relA BINDING SITE 1 and relA BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit relA, a GAM353678 bacterial target gene which is associated with Mycobacterium tuberculosis H37Rv infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Mycobacterium tuberculosis H37Rv infection and associated clinical conditions</p>	A

GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	risA	Bordetella pertussis	GAM353678 is a human miRNA-like oligonucleotide, which targets trespone regulator protein (risA, NC_002929 from 3765257 to 3765991 (-)), a bacterial target gene encoded by the Bordetella pertussis genome, as part of an anti-bacterial host defense mechanism. risA BINDING SITE 1 and risA BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the risA gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of risA BINDING SITE 1 and risA BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit risA, a GAM353678 bacterial target gene which is associated with Bordetella pertussis infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Bordetella pertussis infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	rpsT	Pseudomonas putida KT2440	GAM353678 is a human miRNA-like oligonucleotide, which targets ribosomal protein S20 (rpsT, NC_002947 from 707068 to 707346 (-)), a bacterial target gene encoded by the Pseudomonas putida KT2440 genome, as part of an anti-bacterial host defense mechanism. rpsT BINDING SITE 1 and rpsT BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the rpsT gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of rpsT BINDING SITE 1 and rpsT BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit rpsT, a GAM353678 bacterial target gene which is associated with Pseudomonas putida KT2440 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Pseudomonas putida KT2440 infection and associated clinical conditions	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	ruvB	Yersinia pestis	GAM353678 is a human miRNA-like oligonucleotide, which targets Holliday junction DNA helicase (ruvB, NC_003143 from 2336449 to 2337453 (-)), a bacterial target gene encoded by the Yersinia pestis genome, as part of an anti-bacterial host defense mechanism. ruvB BINDING SITE 1 and ruvB BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the ruvB gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of ruvB	A

					<p>BINDING SITE 1 and ruvB BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit ruvB, a GAM353678 bacterial target gene which is associated with <i>Yersinia pestis</i> infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Yersinia pestis</i> infection and associated clinical conditions</p>	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	ruvB	<i>Yersinia pestis</i> KIM	<p>GAM353678 is a human miRNA-like oligonucleotide, which targets Holliday junction helicase subunit A (ruvB, NC_004088 from 2482031 to 2483035 (-)), a bacterial target gene encoded by the <i>Yersinia pestis</i> KIM genome, as part of an anti-bacterial host defense mechanism. ruvB BINDING SITE 1 and ruvB BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the ruvB gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of ruvB BINDING SITE 1 and ruvB BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit ruvB, a GAM353678 bacterial target gene which is associated with <i>Yersinia pestis</i> KIM infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Yersinia pestis</i> KIM infection and associated clinical conditions</p>	A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	selB	<i>Pseudomonas putida</i> KT2440	<p>GAM353678 is a human miRNA-like oligonucleotide, which targets selenocysteine-specific translation elongation factor (selB, NC_002947 from 582133 to 584055 (+)), a bacterial target gene encoded by the <i>Pseudomonas putida</i> KT2440 genome, as part of an anti-bacterial host defense mechanism. selB BINDING SITE is a bacterial target binding site that is found in the 3' untranslated region of mRNA encoded by the selB gene, corresponding to a target binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of selB BINDING SITE, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit selB, a GAM353678 bacterial target gene which is associated with <i>Pseudomonas putida</i> KT2440 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Pseudomonas putida</i> KT2440 infection and associated clinical</p>	A

				conditions	
GAM35 3678	CAGCAGCA CACTGTGG TTTGTA	Human	SERP1 Human NH 1	GAM353678 is a human miRNA-like oligonucleotide, which targets a human Serine proteinase inhibitor clade H (heat shock prote in 47) member 1; (SERPINH1, Accession number: NM_001235) as pa rt of a host response mechanism associated with a Escherichia coli CFT073, Streptococcus pneumoniae R6, Streptococcus pneumo niae TIGR4, Streptococcus pyogenes M1 GAS, Streptococcus pyoge nes MGAS315, Streptococcus pyogenes MGAS8232 and Streptococcus pyogenes SSI-1 infections. SERPINH1 BINDING SITE 1 and SERPINH1 BINDING SITE 2 are human target binding sites that are found in the untranslated region s of mRNA encoded by the SERPINH1 gene, corresponding to targ e binding sites such as BINDING SITE I, BINDING SITE II or BIN DING SITE III of Fig. 1. Additionally, using the binding site prediction system of the present invention GAM353678-A binds t o sequences on orthologous UTR of rat (NM_017173). The nucleoti de sequences of SERPINH1 BINDING SITE 1 and SERPINH1 BINDING S ITE 2, and the complementary secondary structure to the nucleo tide sequence of GAM353678 RNA are set forth in Tables 6-7, be reb y incorporated herein. Another function of GAM353678 is to inhibit SERPINH1, a GAM353 678 human target gene which encodes a heat shock protein and s erpin, that may function as a chaperone for procollagen in the ER. SERPINH1 is associated with Escherichia coli CFT073, Stre ptococcus pneumoniae R6, Streptococcus pneumoniae TIGR4, Strep tococcus pyogenes M1 GAS, Streptococcus pyogenes MGAS315, Stre ptococcus pyogenes MGAS8232 and Streptococcus pyogenes SSI-1 i nfections, and therefore GAM353678 is associated with the abov ementioned infections, as part of a host response mechanism. A cordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Escherichia coli CFT073, Streptoco cus pneumoniae R6, Streptococcus pneumoniae TIGR4, Streptococ cus pyogenes M1 GAS, Streptococcus pyogenes MGAS315, Streptoco cus pyogenes MGAS8232 and Streptococcus pyogenes SSI-1 infect ions and associated clinical conditions. The function of SERPINH1 and its association with various dise ases and clinical conditions has been established by previous studies, as described hereinabove with reference to GAM839.	A
GAM35 3678	CAGCAGCA CACTGTGG TTTGTA	Human	sitD Shigella flexneri 2a str. 3 01	GAM353678 is a human miRNA-like oligonucleotide, which targets Iron transport protein, inner membrane component (sitD, NC_00 4337 from 1405360 to 1406217 (-)), a bacterial target gene encoded by the Shigella flexneri 2a str. 301 genome, as part of an anti-bacterial host defense mechanism. sitD BINDING SITE 1 and sitD BINDING SITE 2 are bacterial targ et binding sites that are found in the untranslated regions of mRNA encoded by the sitD gene, corresponding to target	A

GAM35 3678	CAGCAGCA CACTGTGG TTTGTGA	Human	sitD	Shigella flexneri 2a str. 2 457T	<p>binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of sitD BINDING SITE 1 and sitD BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit sitD, a GAM353678 bacterial target gene which is associated with Shigella flexneri 2a str. 301 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Shigella flexneri 2a str. 301 infection and associated clinical conditions</p> <p>GAM353678 is a human miRNA-like oligonucleotide, which targets Iron transport protein, inner membrane component (sitD, NC_004741 from 1904666 to 1905523 (+)), a bacterial target gene encoded by the Shigella flexneri 2a str. 2457T genome, as part of an anti-bacterial host defense mechanism. sitD BINDING SITE 1 and sitD BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the sitD gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of sitD BINDING SITE 1 and sitD BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit sitD, a GAM353678 bacterial target gene which is associated with Shigella flexneri 2a str. 2457T infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Shigella flexneri 2a str. 2457T infection and associated clinical conditions</p>	A
GAM35 3678	CAGCAGCA CACTGTGG TTTGTGA	Human	speD	Salmonella enterica enterica serovar Typhi Ty 2	<p>GAM353678 is a human miRNA-like oligonucleotide, which targets S-adenosylmethionine decarboxylase proenzyme (speD, NC_004631 from 196380 to 197174 (-)), a bacterial target gene encoded by the Salmonella enterica enterica serovar Typhi Ty2 genome, as part of an anti-bacterial host defense mechanism. speD BINDING SITE 1 and speD BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the speD gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of speD BINDING SITE 1 and speD BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit speD, a GAM353678 bacterial target gene which is associated with Salmonella enterica enterica serovar Typhi Ty2 infection, as part of an anti-</p>	A

				bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Salmonella enterica enterica</i> serovar Typhi Ty2 infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	speD	<i>Salmonella enterica enterica</i> serovar Typhi	<p>GAM353678 is a human miRNA-like oligonucleotide, which targets S-adenosylmethionine decarboxylase proenzyme (speD, NC_003198 from 196389 to 197183 (-)), a bacterial target gene encoded by the <i>Salmonella enterica enterica</i> serovar Typhi genome, as part of an anti-bacterial host defense mechanism. speD BINDING SITE 1 and speD BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the speD gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of speD BINDING SITE 1 and speD BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit speD, a bacterial target gene which is associated with <i>Salmonella enterica enterica</i> serovar Typhi infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Salmonella enterica enterica</i> serovar Typhi infection and associated clinical conditions</p>
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	speD	<i>Salmonella typhimurium</i> LT2	<p>GAM353678 is a human miRNA-like oligonucleotide, which targets S-adenosylmethionine decarboxylase (speD, NC_003197 from 194201 to 194995 (-)), a bacterial target gene encoded by the <i>Salmonella typhimurium</i> LT2 genome, as part of an anti-bacterial host defense mechanism. speD BINDING SITE 1 and speD BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the speD gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of speD BINDING SITE 1 and speD BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit speD, a bacterial target gene which is associated with <i>Salmonella typhimurium</i> LT2 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Salmonella typhimurium</i> LT2 infection and associated clinical conditions</p>
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	ssb	<i>Pseudomonas putida</i> KT2440	<p>GAM353678 is a human miRNA-like oligonucleotide, which targets single-stranded DNA-binding protein (ssb, NC_002947 from 571027 to 571572 (+)), a bacterial target gene encoded by the</p>

<p><i>Pseudomonas putida</i> KT2440 genome, as part of an anti-bacterial host defense mechanism. <i>ssb</i> BINDING SITE 1 and <i>ssb</i> BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the <i>ssb</i> gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of <i>ssb</i> BINDING SITE 1 and <i>ssb</i> BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit <i>ssb</i>, a <i>Pseudomonas putida</i> bacterial target gene which is associated with <i>Pseudomonas putida</i> KT2440 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Pseudomonas putida</i> KT 2440 infection and associated clinical conditions</p>					A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	<i>ssbB</i>	Escherichia coli CFT073	
<p>GAM353678 is a human miRNA-like oligonucleotide, which targets Protein <i>ssbB</i> (<i>ssbB</i>, NC_004431 from 2922456 to 2923241 (-)), a bacterial target gene encoded by the <i>Escherichia coli</i> CFT 073 genome, as part of an anti-bacterial host defense mechanism. <i>ssbB</i> BINDING SITE 1 and <i>ssbB</i> BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the <i>ssbB</i> gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of <i>ssbB</i> BINDING SITE 1 and <i>ssbB</i> BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit <i>ssbB</i>, a <i>Pseudomonas putida</i> bacterial target gene which is associated with <i>Escherichia coli</i> CFT073 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Escherichia coli</i> CFT073 infection and associated clinical conditions</p>					A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	<i>tofA</i>	Bordetella pertussis	
<p>GAM353678 is a human miRNA-like oligonucleotide, which targets tracheal colonization factor precursor (<i>tofA</i>, NC_002929 from 1264436 to 1266379 (+)), a bacterial target gene encoded by the <i>Bordetella pertussis</i> genome, as part of an anti-bacterial host defense mechanism. <i>tofA</i> BINDING SITE 1 and <i>tofA</i> BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the <i>tofA</i> gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of <i>tofA</i> BINDING SITE 1 and <i>tofA</i> BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678</p>					A
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	<i>tofA</i>	Bordetella pertussis	

				<p>RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit <i>tcdA</i>, a GAM353678 bacterial target gene which is associated with <i>Bordetella pertussis</i> infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Bordetella pertussis</i> infection and associated clinical conditions</p>	
GAM353678	CAGCAGCA CACTGTGG TTTGTGTA	Human	truA	<p>Mycobacterium leprae</p> <p>GAM353678 is a human miRNA-like oligonucleotide, which targets probable pseudouridylate synthase (<i>truA</i>, NC_002677 from 234 3329 to 2344078 (-)), a bacterial target gene encoded by the <i>Mycobacterium leprae</i> genome, as part of an anti-bacterial host defense mechanism. <i>truA</i> BINDING SITE 1 and <i>truA</i> BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the <i>truA</i> gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of <i>truA</i> BINDING SITE 1 and <i>truA</i> BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit <i>truA</i>, a GAM353678 bacterial target gene which is associated with <i>Mycobacterium leprae</i> infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Mycobacterium leprae</i> infection and associated clinical conditions</p>	A
GAM353678	CAGCAGCA CACTGTGG TTTGTGTA	Human	truncated fmbB	<p>Staphylococcus aureus subsp. aureus MW2</p> <p>GAM353678 is a human miRNA-like oligonucleotide, which targets truncated FmbB protein (truncated <i>fmbB</i>, NC_003923 from 2238 083 to 2240143 (-)), a bacterial target gene encoded by the <i>Staphylococcus aureus</i> subsp. <i>aureus</i> MW2 genome, as part of an anti-bacterial host defense mechanism. truncated <i>fmbB</i> BINDING SITE 1 and truncated <i>fmbB</i> BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the truncated <i>fmbB</i> gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of truncated <i>fmbB</i> BINDING SITE 1 and truncated <i>fmbB</i> BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit truncated <i>fmbB</i>, a GAM353678 bacterial target gene which is associated with <i>Staphylococcus aureus</i> subsp. <i>aureus</i> MW2 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Staphylococcus aureus</i> subsp. <i>aureus</i> MW2 infection and associated</p>	A

				clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	uhpA	Yersinia pestis	A
				GAM353678 is a human miRNA-like oligonucleotide, which targets two-component system response regulator (uhpA, NC_003143 from 4522790 to 4523380 (-)), a bacterial target gene encoded by the Yersinia pestis genome, as part of an anti-bacterial host defense mechanism. uhpA BINDING SITE 1 and uhpA BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the uhpA gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of uhpA BINDING SITE 1 and uhpA BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit uhpA, a GAM353678 bacterial target gene which is associated with Yersinia pestis infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Yersinia pestis infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	ung	Haemophilus influenzae Rd	A
				GAM353678 is a human miRNA-like oligonucleotide, which targets uracil DNA glycosylase (ung, NC_000907 from 18676 to 19335 (+)), a bacterial target gene encoded by the Haemophilus influenzae Rd genome, as part of an anti-bacterial host defense mechanism. ung BINDING SITE 1 and ung BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the ung gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of ung BINDING SITE 1 and ung BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit ung, a GAM353678 bacterial target gene which is associated with Haemophilus influenzae Rd infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of Haemophilus influenzae Rd infection and associated clinical conditions	
GAM353678	CAGCAGCA CACTGTGG TTTGTA	Human	vanB	Pseudomonas aeruginosa PA01	A
				GAM353678 is a human miRNA-like oligonucleotide, which targets vanillate O-demethylase oxidoreductase (vanB, NC_002516 from 5504120 to 5505073 (+)), a bacterial target gene encoded by the Pseudomonas aeruginosa PA01 genome, as part of an anti-bacterial host defense mechanism. vanB BINDING SITE 1 and vanB BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the vanB gene, corresponding to target binding sites such as BINDING SITE I,	

GAM353678 CAGCAGCA CACTGTGG TTTGTA	Human yabO	Escherichia coli CFT073	<p>BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of vanB BINDING SITE 1 and vanB BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit vanB, a GAM353678 bacterial target gene which is associated with <i>Pseudomonas aeruginosa</i> PA01 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Pseudomonas aeruginosa</i> PA01 infection and associated clinical conditions</p>	A
GAM353678 CAGCAGCA CACTGTGG TTTGTA	Human yciE	Escherichia coli CFT073	<p>GAM353678 is a human miRNA-like oligonucleotide, which targets Ribosomal large subunit pseudouridine synthase A (yabO, NC_004431 from 61489 to 62148 (-)), a bacterial target gene encoded by the <i>Escherichia coli</i> CFT073 genome, as part of an anti-bacterial host defense mechanism. yabO BINDING SITE 1 and yabO BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the yabO gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of yabO BINDING SITE 1 and yabO BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit yabO, a GAM353678 bacterial target gene which is associated with <i>Escherichia coli</i> CFT073 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis, prevention and treatment of <i>Escherichia coli</i> CFT073 infection and associated clinical conditions</p> <p>GAM353678 is a human miRNA-like oligonucleotide, which targets Protein yciE (yciE, NC_004431 from 1558641 to 1559147 (-)), a bacterial target gene encoded by the <i>Escherichia coli</i> CFT073 genome, as part of an anti-bacterial host defense mechanism. yciE BINDING SITE 1 and yciE BINDING SITE 2 are bacterial target binding sites that are found in the untranslated regions of mRNA encoded by the yciE gene, corresponding to target binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III of Fig. 1. The nucleotide sequences of yciE BINDING SITE 1 and yciE BINDING SITE 2, and the complementary secondary structure to the nucleotide sequence of GAM353678 RNA are set forth in Tables 6-7, hereby incorporated herein. Another function of GAM353678 is to inhibit yciE, a GAM353678 bacterial target gene which is associated with <i>Escherichia coli</i> CFT073 infection, as part of an anti-bacterial host defense mechanism. Accordingly, the utilities of GAM353678 include the diagnosis,</p>	A

prevention and treatment of Escherichia coli CPT07 3 infection and associated clinical conditions

Replace paragraph 0160 with the following paragraph.

Studies documenting the well known correlations between each of a plurality of GAM TARGET GENES that are described by Fig.1 and the known gene functions and related diseases are listed in Table 9, hereby incorporated herein. Specifically, in Table 9, lines 6046-6059 describes references of GAM target genes, as set forth in SEQ ID NO:348 in Table 8.

After paragraph 0160, add the following Table 9, paragraph, Table 11, paragraph, Table 12, paragraph, and Table 13.

Table 9:

TARGET	TARGET ORGANISM	REFERENCES
=====	=====	=====
MGAT5	Human	Demetriou, M.; Granovsky, M.; Quaggin, S.; Dennis, J. W.: Negative regulation of T-cell activation and autoimmunity by Mgat5 N-glycosylation. Nature 409: 733-739, 2001.
MGAT5	Human	Granovsky, M.; Fata, J.; Pawling, J.; Muller, W. J.; Khokha, R.; Dennis, J. W.: Suppression of tumor growth and metastasis in Mgat5-deficient mice. Nature Med.6: 306-12, 2000.
MGAT5	Human	Saito, H.; Nishikawa, A.; Gu, J.; Ihara, Y.; Soejima, H.; Wada, Y.; Sekiya, C.; Hiikawa, N.; Taniguchi, N.: cDNA cloning and chromosomal mapping of human N-acetyl glucosaminyltransferase V+. Biochem. Biophys. Res. Commun. 198: 318-327, 1994.

Table 11, lines 275482-275565, shows data of GAM RNA SEQ ID NO:348 printed on microarray chip probes, as described in detail in Fig.17.

Table 11

PROBE SEQUENCE	PROBE TYPE	GAM RNA SEQ ID/ MIR NAME	GAM RNA/MIR SEQUENCE	LIB RARY	SIG NAL	BACKG ROUND Z-SCO RE	MISM ATCH Z-SCO RE
CCACGACGAC ACTGTGGTTTG TACGCGATCCG TTATCGTTCCG TATCGAACGTA ACGAT	Predicted	348	CAGCAGCACACTGTGGTTTGTA	A2	638	4.2	3.2
CCACGACGAC	Predicted	348	CAGCAGCACACTGTGGTTTGTA	D2	9435	16.6	20.9

ACTGTGGTTTG TACGGATCCG TTATCGTTCCG TATCGAACGTA ACGAT							
CCCAGCAGCAC Predicted ACTGTGGTTTG TACGGATCCG TTATCGTTCCG TATCGAACGTA ACGAT	348	CAGCAGCACACTGTGGTTTGTA	E1	25910	14.8	27.5	
CCCAGCAGCAC Predicted ACTGTGGTTTG TACGGATCCG TTATCGTTCCG TATCGAACGTA ACGAT	348	CAGCAGCACACTGTGGTTTGTA	F1	65518	12.0	30.2	
CCCAGCAGCAC Predicted ACTGTGGTTTG TACGGATCCG TTATCGTTCCG TATCGAACGTA ACGAT	348	CAGCAGCACACTGTGGTTTGTA	G1	65518	10.1	29.3	
CCCAGCAGCAC Predicted ACTGTGGTTTG TACGGATCCG TTATCGTTCCG TATCGAACGTA ACGAT	348	CAGCAGCACACTGTGGTTTGTA	H1	37067	9.9	28.2	
CCCAGCAGCAC Predicted ACTGTGGTTTG TACGGATCCG TTATCGTTCCG TATCGAACGTA ACGAT	348	CAGCAGCACACTGTGGTTTGTA	A2	606	3.7	3.2	
CCCAGCAGCAC Predicted ACTGTGGTTTG TACGGATCCG TTATCGTTCCG TATCGAACGTA ACGAT	348	CAGCAGCACACTGTGGTTTGTA	D2	7549	15.4	19.5	
CCCAGCAGCAC Predicted ACTGTGGTTTG TACGGATCCG TTATCGTTCCG TATCGAACGTA ACGAT	348	CAGCAGCACACTGTGGTTTGTA	E1	20239	13.8	25.3	
CCCAGCAGCAC Predicted ACTGTGGTTTG TACGGATCCG TTATCGTTCCG TATCGAACGTA ACGAT	348	CAGCAGCACACTGTGGTTTGTA	F1	65518	12.0	29.3	
CCCAGCAGCAC Predicted ACTGTGGTTTG TACGGATCCG TTATCGTTCCG TATCGAACGTA ACGAT	348	CAGCAGCACACTGTGGTTTGTA	G1	65518	10.1	28.0	
CCCAGCAGCAC Predicted ACTGTGGTTTG TACGGATCCG TTATCGTTCCG TATCGAACGTA ACGAT	348	CAGCAGCACACTGTGGTTTGTA	H1	27597	9.2	25.8	

TACGGATCGTT
ATAACGATCGG
GTATCGAAGCT
AACGA

Table 12, line 177, shows data relating to GAM RNA SEQ ID NO:348 that were validated by means of Wet Laboratory.

Table 12

GAM RNA SEQUENCE	VALIDATION METHOD	SIGNAL	BACKGROUND Z-SCORE	MISMATCH Z-SCORE	GAM RNA SEQ-ID
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CAGCAGCACACTGGTTTGTGA	Chip strong	65518	16.623587	30.172779	348

Table 13, lines 3-42, 47-69, 84-121, 143-179, 187-207, 210-256, 264-478 shows sequence data of GAMs associated with different bacterial infections.

Table 13

ROW#	INFECTION NAME	SEQ ID NOS OF GAMs ASSOCIATED WITH INFECTION
=====	=====	=====
2	Bordetella pertussis	1, 6, 10, 11, 12, 13, 16, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 33, 34, 37, 41, 42, 43, 44, 47, 48, 49, 50, 52, 53, 54, 55, 57, 58, 59, 60, 63, 65, 66, 67, 68, 69, 70, 71, 75, 76, 77, 79, 84, 86, 87, 88, 89, 91, 94, 96, 97, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 117, 119, 120, 121, 122, 123, 125, 126, 127, 130, 131, 132, 133, 137, 138, 139, 140, 141, 142, 145, 147, 149, 150, 151, 154, 155, 156, 157, 158, 160, 161, 162, 164, 165, 166, 167, 168, 170, 171, 172, 173, 174, 175, 176, 177, 179, 180, 181, 183, 184, 185, 188, 191, 195, 196, 197, 204, 205, 211, 212, 214, 215, 216, 219, 220, 222, 225, 228, 230, 231, 233, 237, 239, 241, 242, 243, 244, 250, 251, 253, 262, 264, 265, 266, 268, 271, 272, 274, 276, 277, 280, 281, 282, 284, 285, 287, 288, 289, 290, 293, 294, 296, 297, 299, 300, 301, 302, 304, 306, 308, 310, 312, 317, 318, 321, 322, 324, 326, 327, 329, 330, 332, 333, 334, 335, 336, 339, 340, 342, 343, 345, 348, 349, 350, 351, 352, 353, 355, 356, 357, 358, 360, 361, 362, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 378, 380, 381, 382, 383, 384, 385 and 49788-55666.
3	Brucella suis	1, 6, 10, 11, 12, 13, 14, 16, 18, 19, 21, 23, 27, 32, 35, 37, 39, 40, 42, 47, 48, 49, 50, 52, 53, 58, 62, 63, 65, 68, 70, 71, 77, 79, 80, 85, 86, 89, 90, 98, 102, 105, 107, 108, 109, 111, 112, 114, 115, 119, 120, 124, 125, 121, 122, 123, 126, 132, 138, 141, 142, 143, 150, 151, 152, 154, 155, 156, 157, 158, 160, 161, 162, 164, 166, 168, 171, 172, 173, 175, 176, 177, 180, 181, 183, 185, 186, 190, 195, 198, 199, 200, 201, 205, 207, 211, 212, 214, 215, 217, 218, 219, 220, 221, 222, 225, 229, 230, 231, 233, 236, 237, 240, 241, 243, 244, 250, 251, 256, 258, 263, 264, 265, 266, 270, 277, 279, 280, 281, 282, 285, 287, 289, 290, 293, 294, 295, 297, 300, 302, 303, 306, 308, 310, 312, 315, 318, 319, 320, 321, 330, 331, 333, 334, 335, 342, 343, 347, 348, 349, 353, 354, 356, 357, 360, 361, 364, 365, 366, 368, 369, 370, 371, 373, 374, 375, 377, 381, 382, 384 and 55667-60259.
4	Chlamydia Trachomatis	2, 3, 4, 6, 7, 8, 9, 10, 13, 14, 16, 18, 19, 20, 21, 22, 25, 26, 27, 30, 31, 32, 33, 36, 37, 38, 40, 45, 46, 47, 48, 49, 51, 52, 55, 62, 63, 64, 67, 73, 74, 75, 78, 81, 82, 84, 85, 86, 87, 88, 91, 94, 95, 98, 99, 104, 105, 106, 111, 113, 116, 122, 124, 126, 128, 132, 133, 136, 138, 146, 148, 149, 152, 154, 155, 156, 157, 160, 164, 166, 167, 177, 179, 180, 181, 187, 188, 190, 192, 194, 198, 199, 200, 205, 207, 208, 209, 210, 211, 213, 214, 217,

- 218, 222, 224, 225, 226, 229, 232, 233, 235, 236, 239, 241, 242, 243, 244, 245, 248, 251, 252, 253, 254, 256, 257, 259, 262, 264, 265, 269, 270, 271, 272, 273, 274, 278, 279, 281, 288, 289, 293, 295, 296, 297, 298, 299, 302, 303, 305, 306, 309, 311, 312, 316, 318, 319, 320, 322, 323, 324, 325, 326, 327, 328, 330, 332, 333, 335, 338, 340, 341, 343, 344, 345, 348, 349, 350, 353, 354, 356, 363, 373, 384 and 60260-67437.
- 6 *Chlamydothrix* 3, 5, 6, 8, 9, 10, 13, 17, 20, 21, 22, 23, 25, 27, 28, 31, 32, 33, 37, 39, 45, 46, 47, 48, 50, 52, 55, 62, 63, 64, 66, 67, 69, 73, 74, 82, 84, 85, 88, 89, 90, 91, 92, 95, 101, 102, 104, 105, 111, 114, 124, 125, 126, 128, 143, 146, 152, 159, 160, 161, 164, 165, 166, 168, 177, 178, 181, 187, 189, 190, 192, 194, 201, 203, 205, 207, 208, 209, 212, 213, 214, 217, 218, 221, 223, 224, 227, 232, 233, 234, 236, 238, 239, 241, 242, 243, 244, 245, 247, 248, 252, 257, 258, 259, 260, 262, 263, 271, 272, 274, 275, 279, 281, 282, 283, 286, 289, 295, 297, 298, 299, 302, 305, 306, 309, 311, 312, 314, 319, 323, 324, 325, 326, 327, 330, 333, 338, 340, 343, 344, 345, 346, 348, 349, 350, 352, 353, 354, 356, 363, 377, 382, 383, 384 and 68148-75439.
- 7 *Chlamydothrix* 3, 5, 6, 8, 9, 10, 17, 20, 21, 22, 23, 25, 27, 31, 32, 33, 37, 39, 45, 46, 47, 50, 52, 55, 62, 63, 64, 66, 67, 69, 73, 74, 82, 90, 92, 95, 101, 84, 85, 88, 89, 102, 104, 105, 111, 114, 125, 126, 128, 148, 152, 159, 160, 161, 143, 146, 164, 165, 166, 168, 175, 176, 177, 178, 179, 187, 189, 190, 192, 194, 201, 203, 205, 207, 208, 209, 212, 180, 181, 213, 214, 217, 218, 221, 223, 224, 227, 232, 233, 234, 236, 238, 239, 241, 242, 243, 244, 245, 247, 248, 252, 257, 259, 260, 262, 263, 271, 272, 274, 275, 279, 281, 282, 283, 286, 289, 295, 297, 298, 299, 302, 305, 306, 309, 311, 312, 314, 319, 323, 324, 325, 326, 327, 330, 333, 338, 340, 343, 344, 345, 346, 348, 349, 350, 352, 353, 354, 356, 363, 377, 382, 383, 384 and 75440-82241.
- 10 *Escherichia* 1, 2, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 16, 17, 18, 19, 21, 22, 23, 25, 26, 27, 28, 30, 31, 33, 34, 35, 36, 37, 39, 40, 42, 43, 45, 46, 47, 48, 49, 50, 51, 52, 53, 55, 56, 57, 58, 59, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 75, 76, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 99, 100, 101, 102, 103, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 119, 120, 121, 122, 123, 124, 125, 126, 129, 131, 132, 133, 135, 136, 137, 138, 140, 141, 142, 143, 145, 146, 147, 148, 152, 154, 155, 156, 157, 158, 160, 161, 162, 163, 164, 165, 166, 167, 168, 171, 173, 174, 175, 176, 177, 179, 180, 181, 182, 184, 185, 186, 190, 191, 192, 193, 195, 196, 197, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 220, 221, 222, 223, 224, 225, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 260, 261, 262, 265, 266, 267, 268, 270, 271, 272, 274, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 299, 300, 301, 302, 303, 305, 306, 307, 308, 309, 310, 311, 312, 314, 315, 316, 317, 318, 321, 322, 323, 324, 325, 326, 327, 329, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 343, 344, 345, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 364, 365, 367, 368, 369, 370, 372, 373, 374, 375, 376, 378, 380, 381, 382, 383, 384, 385 and 90623-103607.
- 11 *Haemophilus* 2, 3, 5, 6, 7, 8, 9, 10, 13, 15, 19, 20, 21, 22, 25, 26, 27, 30, 31, 32, 33, 34, 37, 38, 40, 41, 45, 46, 48, 49, 50, 51, 52, 66, 67, 68, 73, 53, 55, 62, 63, 64, 78, 81, 83, 84, 85, 88, 90, 91, 92, 98, 101, 105, 106, 111, 116, 117, 119, 122, 123, 124, 125, 126, 134, 138, 144, 146, 149, 151, 152, 155, 156, 160, 161, 164, 165, 166, 169, 171, 172, 174, 176, 177, 179, 180, 183, 190, 197, 198, 199, 200, 201, 203, 205, 207, 208, 211, 213, 214, 218, 221, 223, 226, 228, 229, 234, 236, 239, 240, 242, 244, 247, 248, 251, 254, 255, 256, 259, 262, 263, 264, 271, 272, 274, 277, 279, 281, 282, 283, 295, 296, 299, 302, 305, 306, 308, 311, 312, 313, 316, 317, 318, 319, 322, 323, 324, 325, 326, 327, 329, 333, 335, 338, 339, 340, 343, 344, 345, 348, 351, 353, 354, 356, 365,

- 368, 371, 375, 377, 379, 380, 385 and 103608-111433.
- 12 *Leptospira interrogans* serovar lai str. 56601 1, 3, 5, 7, 8, 10, 13, 19, 22, 25, 32, 38, 39, 41, 48, 49, 52, 67, 71, 73, 84, 85, 90, 91, 93, 95, 117, 124, 128, 164, 174, 192, 193, 203, 178, 179, 187, 190, 207, 225, 226, 227, 229, 238, 244, 258, 259, 262, 272, 279, 193, 203, 256, 257, 295, 298, 299, 303, 306, 307, 316, 324, 327, 333, 338, 340, 344, 348, 376, 379, 384 and 111434-116384.
- 15 *Mycobacterium bovis* AF2122/9 subsp. *bovis* 7 1, 3, 4, 5, 6, 7, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 31, 32, 33, 36, 37, 39, 41, 42, 43, 44, 45, 46, 47, 48, 50, 51, 53, 56, 55, 57, 58, 59, 73, 75, 76, 60, 61, 62, 71, 64, 65, 66, 67, 68, 69, 70, 77, 78, 79, 80, 83, 84, 86, 87, 88, 89, 100, 101, 102, 90, 91, 93, 96, 97, 99, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 125, 127, 130, 131, 132, 133, 134, 135, 137, 138, 139, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 165, 166, 167, 168, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 183, 184, 185, 188, 189, 190, 191, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 210, 211, 212, 213, 214, 215, 216, 218, 219, 220, 222, 225, 230, 231, 233, 236, 237, 239, 240, 241, 242, 243, 244, 245, 246, 250, 251, 252, 253, 254, 255, 256, 257, 261, 262, 263, 264, 265, 266, 267, 268, 270, 271, 273, 276, 277, 278, 280, 281, 282, 283, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 296, 297, 299, 300, 302, 303, 304, 305, 306, 308, 310, 312, 313, 314, 315, 318, 320, 321, 322, 323, 324, 325, 326, 327, 329, 330, 332, 333, 334, 335, 336, 337, 341, 342, 345, 346, 347, 348, 349, 350, 351, 352, 353, 355, 356, 357, 358, 360, 361, 362, 364, 365, 366, 367, 369, 370, 371, 372, 373, 374, 375, 376, 378, 380, 381, 382, 383, 384, 385 and 127919-137561.
- 16 *Mycobacterium leprae* 3, 4, 5, 6, 7, 12, 13, 14, 15, 18, 19, 21, 22, 23, 24, 26, 29, 31, 32, 33, 36, 37, 39, 41, 42, 43, 45, 46, 47, 48, 49, 50, 53, 54, 68, 69, 70, 57, 59, 62, 65, 71, 73, 74, 75, 76, 78, 81, 83, 84, 86, 90, 94, 96, 98, 101, 103, 106, 107, 109, 110, 111, 112, 113, 114, 115, 116, 118, 119, 120, 121, 123, 131, 133, 134, 135, 137, 142, 143, 144, 145, 146, 147, 149, 154, 156, 157, 158, 159, 161, 162, 163, 165, 166, 167, 171, 172, 173, 174, 175, 176, 179, 183, 184, 185, 187, 188, 189, 190, 193, 196, 197, 198, 199, 200, 201, 202, 204, 205, 206, 211, 212, 214, 215, 216, 218, 219, 220, 221, 223, 224, 225, 228, 230, 231, 232, 233, 234, 235, 236, 237, 241, 242, 243, 245, 249, 250, 251, 253, 254, 256, 258, 261, 263, 265, 267, 268, 269, 271, 274, 276, 277, 280, 281, 284, 288, 289, 290, 291, 293, 294, 295, 296, 297, 299, 300, 301, 302, 303, 305, 306, 307, 309, 310, 311, 312, 313, 314, 315, 318, 320, 321, 323, 324, 327, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 343, 345, 346, 347, 348, 349, 353, 355, 356, 357, 358, 360, 361, 364, 365, 368, 369, 370, 371, 372, 374, 375, 376, 377, 378, 380, 381, 382, 383 and 137562-144598.
- 18 *Mycobacterium tuberculosis* H37Rv 1, 3, 4, 5, 6, 7, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 31, 32, 33, 37, 39, 41, 42, 43, 50, 51, 52, 45, 46, 47, 48, 53, 54, 55, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 73, 75, 76, 77, 78, 79, 80, 83, 84, 86, 87, 88, 89, 90, 91, 93, 94, 96, 97, 99, 100, 101, 102, 103, 104, 105, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 125, 127, 130, 131, 132, 133, 134, 135, 137, 138, 139, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 165, 166, 167, 168, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 183, 184, 185, 188, 189, 190, 191, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 210, 211, 212, 213, 214, 215, 216, 218, 219, 220, 222, 225, 230, 231, 233, 234, 236, 237, 239, 240, 241, 242, 243, 244, 245, 246, 250, 251, 252, 253, 254, 255, 256, 257, 261, 262, 263, 264, 265, 266, 267, 268, 270, 271, 272, 273, 274, 276, 277, 278, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 296, 297, 298, 299, 300, 302, 303, 304,

- 305, 306, 308, 310, 312, 313, 314, 315, 318, 320, 321, 323, 324, 325, 326, 327, 329, 330, 331, 332, 333, 334, 335, 336, 337, 341, 342, 345, 346, 347, 348, 349, 350, 351, 352, 353, 355, 356, 357, 358, 360, 361, 362, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 378, 380, 381, 382, 383, 384, 385 and 146807-155497.
- 20 *Neisseria meningitidis* Z2491 1, 6, 7, 8, 10, 12, 15, 17, 21, 22, 26, 28, 30, 37, 39, 40, 45, 49, 52, 56, 58, 60, 62, 63, 67, 70, 76, 86, 89, 90, 91, 96, 98, 102, 103, 105, 107, 108, 109, 111, 112, 113, 114, 115, 122, 123, 124, 125, 126, 127, 133, 138, 141, 142, 143, 145, 147, 148, 149, 152, 157, 158, 164, 165, 166, 170, 171, 175, 176, 178, 181, 183, 187, 189, 191, 203, 211, 218, 219, 220, 221, 222, 225, 229, 230, 231, 237, 239, 243, 245, 247, 248, 251, 253, 254, 256, 257, 258, 259, 264, 265, 268, 273, 281, 282, 283, 285, 287, 289, 290, 293, 294, 295, 297, 300, 302, 306, 308, 314, 315, 316, 319, 321, 322, 325, 327, 329, 332, 333, 334, 338, 340, 341, 344, 346, 348, 349, 350, 351, 354, 355, 356, 365, 371, 372, 375, 376, 380, 381, 382, 384 and 155834-160603.
- 21 *Pseudomonas aeruginosa* PA01 1, 2, 6, 10, 11, 12, 13, 14, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 33, 34, 35, 36, 37, 41, 42, 56, 43, 45, 46, 48, 49, 50, 52, 54, 55, 57, 58, 59, 60, 62, 63, 64, 76, 77, 78, 79, 81, 85, 86, 87, 88, 89, 90, 91, 94, 95, 96, 97, 99, 100, 101, 102, 103, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 130, 131, 134, 137, 138, 139, 140, 141, 142, 144, 147, 149, 150, 151, 152, 154, 155, 156, 157, 158, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 179, 180, 181, 183, 184, 185, 188, 190, 192, 193, 194, 195, 196, 197, 202, 204, 205, 208, 210, 211, 212, 213, 214, 215, 216, 218, 220, 222, 225, 228, 229, 230, 231, 232, 233, 236, 237, 241, 242, 243, 244, 250, 251, 253, 258, 262, 264, 265, 266, 267, 268, 270, 271, 272, 273, 274, 276, 277, 280, 281, 282, 283, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 296, 297, 298, 299, 300, 301, 302, 306, 312, 314, 318, 319, 320, 321, 323, 324, 325, 327, 329, 330, 331, 333, 334, 335, 336, 339, 340, 341, 342, 343, 345, 347, 348, 349, 350, 351, 352, 353, 355, 356, 357, 358, 360, 361, 362, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 378, 380, 381, 382, 383, 384 and 160604-170274.
- 22 *Pseudomonas K putida* T2440 1, 5, 7, 9, 10, 11, 12, 13, 14, 16, 18, 19, 23, 24, 25, 26, 27, 28, 29, 31, 33, 34, 36, 37, 38, 39, 41, 42, 43, 44, 45, 46, 47, 49, 50, 51, 52, 53, 54, 55, 57, 58, 59, 61, 64, 65, 66, 68, 69, 70, 71, 73, 76, 84, 85, 86, 88, 89, 91, 94, 98, 99, 101, 102, 103, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 117, 118, 119, 120, 121, 122, 123, 125, 126, 131, 132, 133, 134, 135, 137, 138, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 166, 167, 168, 171, 172, 173, 174, 175, 176, 177, 179, 180, 181, 183, 184, 185, 187, 190, 191, 193, 195, 196, 197, 202, 204, 205, 207, 211, 212, 214, 215, 216, 220, 221, 222, 225, 228, 229, 230, 231, 232, 233, 234, 236, 237, 240, 241, 242, 243, 244, 248, 250, 251, 253, 255, 258, 264, 265, 266, 267, 270, 271, 272, 274, 276, 277, 280, 281, 282, 283, 284, 285, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 308, 310, 312, 313, 314, 316, 317, 318, 320, 321, 322, 323, 324, 327, 329, 333, 334, 335, 336, 337, 342, 343, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 360, 361, 364, 365, 366, 367, 368, 369, 370, 371, 373, 374, 375, 376, 377, 378, 380, 381, 382, 383, 384, 385 and 170275-178543.
- 24 *Salmonella enterica enterica* serovar 1, 2, 3, 4, 6, 7, 8, 9, 10, 11, 12, 13, 16, 17, 18, 19, 20, 21, 22, 23, 25, 26, 27, 28, 30, 31, 32, 33, 35, 37, 38, 39, 51, 40, 42, 43, 45, 46, 47, 48, 49, 50, 52, 55, 56, 57, 58, 59, 60, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 75,

Typ hi	7, 79, 80, 81, 83, 84, 86, 88, 89, 90, 91, 92, 94, 95, 98, 99, 100, 101, 102, 105, 106, 107, 108, 109, 111, 112, 113, 114, 115, 116, 119, 120, 121, 122, 123, 124, 125, 126, 127, 129, 131, 132, 133, 135, 136, 137, 138, 142, 143, 144, 145, 146, 147, 148, 150, 152, 153, 154, 155, 156, 157, 158, 160, 161, 162, 163, 164, 165, 166, 167, 171, 172, 173, 174, 175, 176, 177, 179, 180, 181, 182, 183, 185, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 208, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 225, 226, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 247, 248, 250, 251, 252, 253, 254, 255, 256, 257, 260, 261, 262, 263, 265, 266, 269, 270, 271, 272, 274, 276, 277, 278, 280, 281, 282, 283, 284, 285, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 308, 311, 312, 314, 315, 318, 319, 323, 324, 325, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 351, 352, 353, 354, 355, 356, 357, 358, 360, 361, 364, 365, 366, 367, 369, 370, 371, 373, 374, 375, 376, 378, 379, 380, 381, 382, 383, 384, 385 and 179915-190940.
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